STIC-Biotech/Ch mLib

79027

Fr m:

Mehta, Ashwin

Sent:

Wednesday, October 30, 2002 9:06 AM

To: Subject: STIC-Biotech/ChemLib sequence search

STIC,

Please search the commercial and interference databases for the following from 09/896,186

T 30 7

1) the nucleotide sequence of SEQ ID NO: 23 2) the amino acid sequence of SEQ ID NO: 24

My mail room is 9E12, office 9E07, art unit 1638.

Thank you, Ashwin

Ashwin Mehta United States Patent and Trademark Office Biotechnology Patent Examiner 703-306-4540

Point of Contact
P. Sheppard

Searcherephone number: (703) 308-4499

Phone:______Location:

Date Picked Up:

Date Completed: 11/7/02

Searcher Prep/Review:_____ Clerical:

Online time:

TYPE OF SEARCH:

NA Sequences:_____

Structures:_______Bibliographic:_____

Litigation:

Full text:______
Patent Family:_____
Other:

VENDOR/COST (where applic.)

STN:______

Questel/Orbit:______DRLink:_____

Lexis/Nexis:______Sequence Sys.:______
WWW/Internet:_____

Other (specify):___

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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

VERSION
KEYWORDS
SOURCE
ORGANISM COMMENT REFERENCE AUTHORS RESULT 1 AU226180/c LOCUS ACCESSION DEFINITION TITLE JOURNAL Plant Functional Genomics Research Group RIKEN Genomic Sciences Center, 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Tel: 81-298-36-4359 Fax: 81-298-36-9060 Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
Large scale analysis of Arabidopsis full-length cDNA Unpublished (2002) Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 435)
Cokin Magnoliophyta; Magnoliophyta;
Cokin Magnoliophyta; Magnoliophyta;
Cokin Magnoliophyta;
C AU226180
AU226180 RAFL14 Arabidopsis thaliana cDNA clone RAFL14-14-A20 3', mRNA sequence.
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GI:19740827 Email: mseki@rtc.riken.go.jp An Arabidopsis full-length cDNA library was constructed as reported previously (Seki et al., 1998).cDNA cleaved Contact: Motoaki Seki thale cress. 305-0074, Japan

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RESULT 2
BE659005/c
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                      Unpublished (1999)
Other_ESTs: AM460204 corresponding to Gm
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                                                                               Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Erpelding,J., Raph,C., Shoop,E., Pardinas,J., A Functional Genomics Program for Soybean (NS
                                                                                                                                                                                                                 soybean.
Glycine max
                Contact: Vodkin, L.O. Soybean (NSF 9872565)
                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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/db_xref="taxon:3702"
/clone="RaFL14-14-220"
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2.2e-61;
nes 17;
                                                                               Retzel,E., Khanna,A.,
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for
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                         GTAGGTATTGGAATTGATGGTGACTCTGTGÅAGCTTTTCCATGACTATGGAGTTAGTATC
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                                                                                                             ATTCATTCTGGAATCCCTCAAAATTTACAGCTTTTGCTTGAAGATCCCACAGTCTTGAAG
                                                                                                                                          TTTCATTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAAAG
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Edwin R. Madigan Building,
Tel: (217) 244-6147
Fax: (217) 333-4582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314) 427-3324 or contact:clones@genomesystems.com or info@genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   various tissues and stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,770 from immature seed coats, 3,938 from flowers, and 869 from young pods. The 5' ESTs of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-r1070. The cDNA clones of the reracked Gm-r1070 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel. Center for Computational Genomics and Bioinformatics, University of Minnesota, http://www.cbc.umm.edu/ResearchProjects/Soybean/index.html
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An integrated analysis of the genetics, deve of the cotton fiber Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
ATCATCAAGATAACCTCAAAACCAGCCGCCAATTGCCCCCATTCTATTCTCTCACCCCCGC
                             CAAATCAAATCCCCAATAATATCCGTCGCCAATTGCCTCGTTCCATCACTTCTTCTACAT 264
                                                                                CTTCCTCTGCTGCTCCGACCGTACAAGCTACAACCTCCGTCCATGGCCACGAGGAGGATC 204
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arboreum cDNA clone GA_Ea0013022f, mRNA sequence.
BG441595
BG441595.1 GI:13351247
EST.
EST.
Gossypium arboreum.
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                                                                                                                                                Similarity
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/clone="GA_Ea0013022f"
/clone_lib="Gossypium arboreum
/tissue_type="Fibers isolated f
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                                                                                                                                                                                                           /note="Vector: pBK-CMV; Site_1: 144 c 155 g 217 t
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                                              AW201789 552 bp mRNA linear EST 02-DEC-2001 sf07c10.y1 Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1027-1579 5' similar to TR:Q9Z242 Q9Z242 WRN PROTEIN. ;, mRNA
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SOURCE ORGANISM COMMENT REFERENCE KEYWORDS JOURNAL TITLE AUTHORS Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST E
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1 I (bases 1 to 552)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Tel: 314 286 1800 Fax: 314 286 1810 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Phaseoleae; Pabales; Fabales; Pabaceae; Papilionoideae; Phaseoleae Louis, ŏ Phaseoleae; Beck, C.,

clone

est@watson.wustl lone is available

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                                                                                                                                                                                                                               TTGCGACTGTCCAGATATGTGTAGATAGTAATTATTGTGATGTTATGCATATTTTTCATT
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                                              TTGAGGATCTTTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAAAAAATGGGGCCTTG 726
                                                                                                CTGGGATTGATGGTGATGCTGTGAAGGTTTTTAGAGATTATAACATATCTGTTAAAGGTG
                                                                                                                                                                                                   CTGGAATCCCTCAAAATTTACAGCTTTTGCTTGAAGATCCCACAGTCTTGAAGGTTGGAG
                                                                                                                                                                                                                                                                                                   TAGCAGTGATGCAGATATGTGGTGACACTAGACATTGTCATGTTCTACATCTAATTCATT
TGACGGATCTTTCTTTCATGCTAATCAAAAGCTTGGTGGAGATCATAAGTGGGGTCTTG
                                                                                                                                                 TTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             water. The cotyledons were flash-frozen in liquid nitrogen, then lyophilized for 72 hours. Unequal amounts of mRNA was used for cDNA synthesis. Stratagene's cDNA Synthexix Kit (catalog number 200401) was used to synthesize the cDNA. First- stranded synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was heminethylated. A modification of Stratagene's first-strand synthesis primer was used. An anchor nucleotide (v=A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGAGATAGTTCGAG(T)]18] to anchor the primer at the 5' end of the poly(A) tract. After second- strand synthesis, the cDNA ends were filled in with load and synthesis, the cDNA ends were filled in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   column. The column eluent was then ligated into Stratagene's pBluescript(tm) II XR Predigested vector (pBluescript II SK(+) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). 97% of the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=30). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500 bp cutoff, using GibcoBKL Life Technologies, CDNA Size Fractionation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 which were propagated on paper towels with distilled
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/clone_lib="Gm-c1027"
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/db_xref="taxon:3847"
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TTTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAAAAAATGGGGCCTTGCCTCACTAA
                                                                                          GACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGT----ATCAAAGATGTTGAGGATC 675
                                                                                                                                   ATGCTTCATGGCATCTTTACAAGGTTCTTAAGGACCTTCCTGATGC
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                                                      GACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAATCAAAGATGTTGAGGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K. Isarge scale analysis of Arabidopsis full-length cDNA Unpublished (2002)
Contact: Motoaki Seki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 671)
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AU237507
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Tel: 81-298-36-4359
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RIKEN Genomic Sciences Center
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EST.
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/lab_host="DH10B"
/note="Site_1: BamHI;
109 c 164 g
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/db_xref="taxon:3702"
/clone="RAFL16-31-E24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available through: ResGen, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35801 For further in call: (800)-533-4363 or contact via email: ccu@resgen.com Insert Length: 734 Std Error: 0.00
High quality sequence stop: 417.
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Tel:
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467 bp mRNA linear EST 03-DEC-2001 sm20b11.y1 Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1027-9430 5' similar to SW:WRN_HUMAN Q14191 WERNER SYNDROME
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Fax: 314 286 1810
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Washington University School of Medicine
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AW832139.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                     /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from cotyledons of 3- and 7-day-old williams seedlings which were propagated on paper towels with distilled water. The cotyledons were flash-frozen in liquid nitrogen, then lyophilized for 72 hours. Unequal amounts of mRNA was used for cDNA synthesis. Stratagene's cDNA Synthexix Kit (catalog number 200401) was used to synthesize the cDNA. First- stranded synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was heminathylated.

    a; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    phyta; Magnollophyta; eudicotyledons; core eudicots;
    eurosids I; Fabales; Fabaceae; Papilionoldeae; Phaseoleae;

                  first-strand synthesis primer was used. An anchor nucleotide (V=A, C, or G) was added to the 3′ end of the primer [GAGAGGAGAGAGAGAGAGAGAGTCTCGAG(T)18] to anchor the primer at the 5′ end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shoemaker
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seedlings"
                                                                                                                                                          hemimethylated. A modification of Stratagene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="GENOME SYSTEMS CLONE ID: Gm-c1027-9430"
/clone_lib="Gm-c1027"
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/db_xref="taxon:3847"
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CTTCTTGGTGTCTNTATCAGGCGATTAAAGATCTCCCGGACGC
                                            CTTCATGGCATCTTTACAAGGTTCTTAAGGACCTTCCTGATGC 892
                                                                                       ATTGGGAGGCTCCTGTTTTGTCAAAGGAGCAACTAGAGTATGCTGCAACAGATGCTTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
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BQ799068 LOCUS REFERENCE AUTHORS DEFINITION SOURCE KEYWORDS VERSION ACCESSION RESULT TITLE ORGANISM Abbal, P., Agasse, A., Ageorges, A., Couture, C., Dedaldechamp, F., Delro Hamdi, S., Romieu, C. and Terrier, M. Generation of Expressed Sequence T or seeds) at Various Developmental Vitis vinifera. Vitis vinifera Eukaryota; Viridiplantae; Stro Spermatophyta; Magnoliophyta; BQ799068
EST 1237 Green Grape
CDNA clone GT172E01 3
BQ799068 Vitaceae; вQ799068.1 (bases 1 to 661) Vitis GI:22014034 661 e berries 3', mRNA Streptophyta; Embryophyta; rta; eudicotyledons; core eu bp mRNA linear EST 30-JUL-20: Lambda Zap II Library Vitis vinifera sequence. Delrot,S., Tag from Grape al Stages Atanassova, R., ot, S., Glissant, Berry (skin, pulp Barrieu, F., D., Grimpl eudicots; EST 30-JUL-2002 Grimplet, J., Tracheophyta;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2002)
Contact: Romieu C.
Unite de Recherche des Produits de la Vigne
Institut National de la Recherche Agronomique
place Viala, 34 006 Montpellier Cedex 01, F
Tel: 00-33-(0)4-99-61-28-57
Fax: 00-33-(0)4-99-61-28-57
 Solanum
                                            EST580451 potato roots
end, mRNA sequence.
BM406124
BM406124.1 GI:18257754
                                                                                                          BM406124
               potato.
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33; Conservative
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/dev_stage="green stage"
/note="0rgan: Fruit; Vector: Lambda Zap II; Site_1: Eco R1
/ Site_2: XhOI; Oriented library, construction described in Generation of ESTs from grape Berry (skin, pulp or seeds) at various developmental stages by Terrier,N.,
Ageorges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158
(12): 1575-83 2001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Vitis vinifera"
/cultivar="Shiraz"
/db_xref="taxon:29760"
/clone="GT172E01"
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pred. No. 4.7e-48;
0; Mismatches 141;
                                                                                            Solanum
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                                                            TTGGGGGATTGGGAAGGCTAATGTTATCTAGGGACCAACTACATTATGCTGCTACAGAT
                                                                            CTTGGGAACTGGGAGTTTTATCCTCTGTCAAAGCAGCAGTACAATACGCAGCAACGGAT
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Utterback,T., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C.,
Tanksley,S. and Baker,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="potato roots"
/tlssue_type="roots"
/dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="cPRO26F14"
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/cultivar="Kennebec"
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Pred. No. 1.1e-47;
0; Mismatches 187;
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GCTTTGGAAGATCTTTCCGAACTTGCCAACAAAAAGCTTGATGATCCCAAGAAGTGGAGT
                                 GATGTTGAGGATCTTTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAAAAAATGGGGC 722
                                                                                                   GGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAA 662
                                                                                                                                                                       CATTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAAAGGTA 602
                                                                                                                                                                                                           AAGGCTGCTGTTATGCAGATATGTGGTGACAAGGGTAATTGTTATGTTTTTGCATATCATC
                                                                                                                                                                                                                                                                              GTTGCTCTTGGATTTGACATTGAATGGAAGCCCCACTTTTAGAAGAGGTGTGCCCACCTGGG
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                                                                                                                                         CACTCCGGAATCCCTCAAACTCTGCAATCTCTTGAGGATCCAACTGTTGTGAAGGTG
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Contact: CUGI
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Generation of ESTs from tomato crown gall tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: xho1; Four wk old greenhouse plants were stab inoculated on stem with Agrobacterium tumefaciens C58 (Dr. T.J. Burr Cornell U.). Galls were allowed to develop for another 4 wks, when gall tissue was frozen in liquid nitrogen." a 91 c 126 g 147 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Lycopersicon
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cTOE11B12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="tomato crown gall"
/tissue_type="crown gall"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="crown galls from full-grown plants (8 wks old
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Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available through: ResGen, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35801 For further in call: (800)-533-4363 or contact via email: ccu@resgen.com High quality sequence stop: 423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Public Soybean EST Project Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wylle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurl,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shoemaker, R., Keim, P., V, A., Bolla, B., Marra, M.,
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  est@watson.wustl.edu
  Q
                                                                                                                                                                                         note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from unexpanded leaves and the shoot tips of 2 week old seedling from the cultivar Williams. The 2 week old seedlings were salt stressed in a solution of 500mM NaCl for 3 days prior to harvesting. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI
                                     of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy
                                                                                                                adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction s
                         Shoemaker.
                                                                                                                                                                                                                                                                                                                                                                                                                         old seedling"
                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="GENOME SYSTEMS CLONE ID: /clone_lib="Gm-c1066"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Glycine max"
/db_xref="taxon:3847"
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                                                                                      Contact: Wing RA
Clemson University Genomics
Clemson University
100 Jordan Hall, Clemson, SC
                                                                                                                                        1 (bases 1 to 515)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmo,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, of the cotton fiber Unpublished (2000)
                                                                                                                                                                                                                                                                                                                          BM358892
515 bp mRNA linear GA_Ea0013P02r Gossypium arboreum 7-10 dpa fiber arboreum cDNA clone GA_Ea0013P02r, mRNA sequence
                       Email: rwing@clemson.edu
Total High Quality bases = 415
Seg primer: TAATACGACTCACTATAGGG
                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, developm
of the cotton fiber
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                             BM358991 517 bp mRNA linear EST 09-JAN-2002
GA__Ea0013022r Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA__Ea0013022r, mRNA sequence.
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/clone_lib="Gossypium arboreum
/tissue_type="Fibers isolated i
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/strain="AKA"
/cultivar="8400"
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/note="Vector: pBK-CMV; Site_1:
112 c 109 g 160 t
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Fax:
                                                                  BM731125 55 bp mRNA linear EST 01-MAR-2002 sal68a05.yl Gm-c1061 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1061-4233 5' similar to TR:Q9SVM6 Q9SVM6 HYPOTHETICAL 35.1 KD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total High Quality bases = 327
Seq primer: TAATACGACTCACTATAGGG
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                                                      ;, mRNA sequence.
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/db_xref="taxon:29729"
/db_ne="6A__Ea0013022r"
/clone_11b="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-1
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112 c 108 g 161 t 1 others
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/strain="AKA"
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                              GTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGTAATTATTGTGATGTT
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GTTCCTCCCGGAAAGGTAGCAGTGATGCAGATATGTGGTGACACTAGACATTGTCATGTT
                                                                                                                        GACATGATGCAAACTGCAATTGGATTTGACATTGAGTGGAAACCCACCTTCAGAAAAGGT
                                                                                                                                                                                                                                                     TTTGATGCTGTAGAGAAAGCTGCAACAAAGCTCTTACAAATTCTCCAAGAAAAAACGACC
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                                                                                                                                                                                                                                                                                                                                                                                 GATTCAAGAATGACATTGCCTGTAATGAAGTTTAGTGGTCAAATTTCTTATAGCAGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCAATTCTGCTATTCACTATACATTTCCTCTAATTTTTCATTTTTCATCTTGCACAGGC 165
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
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Location/Qualifiers
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This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further in
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="mature flowers of field grown plants"
/lab_host="DH10B"
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/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1061-4233"
/clone_lib="Gm-c1061"
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60.8%;
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GTTAGTATCAAAGATGTTGAGGATCTTTC 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCTTGAAGGTTGGAGCTGGGATTGATGGTGATGCTGTGAAGGTTTTTAGAGATTATAAC
                                                                                                                                  323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bread wheat.
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BJ213300 595 bp mRNA linear EST 04-APR-2002 BJ213300 Y. Ogihara unpublished cDNA library, Wh Triticum aestivum cDNA clone wh21m08 5', mRNA sequence.
BJ213300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 595)
Ogihara, Y. and Murai, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea; Triticeae; Triticum.
                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BJ213300.1 GI:19952807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expressed genes in Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81-559-81-6855
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81-559-81-6856
                                                                                                                                                                                                                    /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin,
Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
70 a 119 c 148 g 157 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Y. Ogihara unpublished
/tissue_type="spike at meiosis"
/dev_stage="Feekes' scale 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4565"
/clone="wh21m08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Triticum aestivum"
/cultivar="Chinese Spring"
                                                                                                                                                15.4%; 58.3%;
                                                                                                                              Score 162; DB 13;
Pred. No. 9.1e-30;
0; Mismatches 225;
                                                                                                                                                                 Length 595;
                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA library,
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RESULT 15
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             621 GACTCTGTGAAGCTTTTCCATGACTATGGAGTTATCAAAGATGTTGAGGATCTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                501 ATATGTGTAGATAGTAATTGTGTGATGTTATGCATATTTTTCATTCTGGTATCCCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTTATCCTCTGTCAAAGCAGCAGTTACAATACGCAGCAACGGATGCTTATGCTTCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAATGGTTACATGTAAAGAGTTGCCAAAGCCTGGCAACATAAGAATGGGAAACTGGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTTTTGTTCTCAAAAAAGCAACTTGAGTATGCTGCTACCGATGCCTACATCTCGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C.M., Fry,W.E. and Baker,B. Generation of ESTs from Potato Leaves Challenged with Phytopht infestans, Compatible Interaction Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Cathy Ronning
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             potato.
Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI433038 499 bp mRNA linear EST 21-AUG-2001 EST535799 P. infestans-challenged leaf Solanum tuberosum cDNA clone PPCAZ86 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 499)
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                                                                                                                                                                                                                                                                                                                                                         primer: M13F-R
/note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site, XhoI; Whole plants were challenged with 450,000 sporangia,ml P. infestans US-1(US 940501) in Biotron (Madison, Wisconsin). Leaf tissue was collected at 1,
                                                                                                                                                                                                  /cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="PPCAZ86"
                                                                                                /clone_lib="p. infestans-challenged
/tissue_type="leaf"
/dev_stage="6 week old"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                              /organism="Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Challenged with Phytophthora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 21-AUG-2001
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BASE COUNT
ORIGIN
Search completed: November Job time: 2052 secs
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Best Local Similarity
                                                                                                                                                                                        288
                                                                                                                           656 TATCAAAGATGTTGAGGATCTTTCAGATTTAG 687
                                                                                                                                                                                                                                                                                                                    536 TATTTTTCATTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACCTTGT 595
                                                                                                                                                                                                                                                                                                                                                                                                                   416 TGGAATAGCTTTTGTTGGCTTGGATATTGAGTGGAGACCAAGTTTTAGAAAAGGTGTTCT 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 AGCTAGGAATTTTTCCAGCAATGAGGTTTGGTGGTAGGATTTTTGTATAGCAAGACTGCTAC 355
                                                                                                 468 TGTGAAGGCTTTGGAAGATCTTTCTGAACTTG 499
                                                                                                                                                                                                                                         596 AAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAG 655
                                                                                                                                                                                                                                                                                          348 TATCATCCACTCTGGAATCCCTCAAACTCTGCAATCTCTTCTTGAGGATCCAACTGTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 AGAGGTGGAGAAATCTGCAGTAGAGCTGTTAAATTTTGTTGAGGAAAAGAAGAAGAAGAAGA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AGTGATGCAGTACCCGGAAATGTCTTTTAAAGGACATGTTATATACAGCAGAACTATTAA 167
                                                                                                                                                                                                                                                                                                                                                                                            ACCTGGGAAGGCCGCTGTTATGCAGATATGTGGTGACAAGGGTAATTGTTATGTTCTGCA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed no signs of HR. Katahdin plants (susceptible to P. infestans US-1) were used as controls and showed infection. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.9%; 62.5%;
                       2, 2002, 15:31:41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 156.8; DB 13; Length 499;
Pred. No. 1.8e-28;
0; Mismatches 147; Indels 0;
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
       4:
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Gapop 10.0 , Gapext 1.0
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1049
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                                                                                                                                                                                                                                                                                                                                   Published_Applications_NA: *
/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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:/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                                                                                                                                                                                                                /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Sequence 10134, A	Sequence 860, App	Sequence 8619, Ap	Sequence 270, App	Sequence 8066, Ap	Sequence 6599, Ap	Sequence 3, Appli	Sequence 5350, Ap	ω		Sequence 3, Appli	Sequence 1, Appli		Sequence 3, Appli	Sequence 20174, A	Sequence 127, App	Sequence 1131, Ap	Description

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	Sequence 30755, A	Sequence 555, App	Sequence 9, Appli	Sequence 9, Appli	Sequence 8070, Ap	Sequence 86, Appl	Sequence 3803, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 3814, Ap	Sequence 3768, Ap	Sequence 9161, Ap		Sequence 1424, Ap	Sequence 3, Appli	Sequence 1156, Ap	Sequence 505, App	Sequence 2534, Ap	'n	Sequence 5436, Ap	Sequence 8615, Ap	-	Sequence 8801, Ap	Sequence 4754, Ap	`

ALIGNMENTS

RESULT 1 US-09-954-456-1131

GENERAL INFORMATION: APPLICANT: Young, F

Sequence 1131, Application US/09954456 Patent No. US20020115057A1

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; SOFTWARE: PatentIn versic
; SEQ ID NO 1131
; LENGTH: 5189
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-455-1131
              Query Match
Best Local Similarity
Matches 272; Conserv
                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                  PRIOR FILING DATE:
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CURRENT APPLICAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using TITLE OF INVENTION: Sets
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US/60/235,863
                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US/60/235,720
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PRIOR FILING DATE: 2000-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
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CURRENT FILING DATE: 2001-09-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/60/235,638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US/60/234,052
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)S: 2276
                                   10.6%;
              Score 111; DB 10;
Pred. No. 2.4e-22;
0; Mismatches 225;
                                                         Length 5189;
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                                                  ; ORGANISM: Homo sapiens
US-09-729-674-127
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US-09-729-674-127
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Query Match
Best Local Similarity
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                                                                                                              SEQ ID NO 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL
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                                                                                                                                                                                     APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jacobs, Kennern
APPLICANT: MCCOy, John M.
APPLICANT: Lavallie Edward R.
                                                                                                                                   SOFTWARE: PatentIn Ver.
                                                                                                                                                PRIOR APPLICATION NUMBER: 09/539,330 PRIOR FILING DATE: 2000-03-30 NUMBER OF SEQ ID NOS: 283
                                                                                  LENGTH: 3149
TYPE: DNA
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Treacy, Maurice
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Evans, Cheryl
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Pred.
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No. 0.
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               10;
               Length 3149;
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US-09-864-761-20174/c
; Sequence 20174, Application
; Patent No. US20020048763A1
; GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HUMAN GENOME-DERIVED TITLE OF INVENTION: GENE EXPRESSION ANAI
                                                                                                                                                                                                                                                                                                                      OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00664
OR APPLICATION NUMBER: PCT/US01/00669
OR APPLICATION NUMBER: PCT/US01/00669
IOR APPLICATION NUMBER: PCT/US01/00665
IOR APPLICATION NUMBER: PCT/US01/00665
IOR FILING DATE: 2001-01-30
IOR FILING DATE: 2001-01-30
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R FILING DATE:
R APPLICATION N
R FILING DATE:
                                                                                                                                                                                                                                                                          FILING DATE: 2001-01-30
PTILING DATE: 2001-01-30
PTILING DATE: 2001-01-30
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PTILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
                                                           APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21 APPLICATION NUMBER: US 09/608,408
                                                                                                                         APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
                                                                                                                                                                                                            FILING DATE: 2001-01-30
                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00662
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Hanzel, David K.
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                                                                                                                                                                 NUMBER: PCT/US01/00661: 2001-01-30
                                      2000-06-30
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TYPE: DNA

TYPE: DNA

ORGANISM: HOMO SapienS
FEATURE:

OTHER INFORMATION: EXPR
OTHER INFORMATION: EXPR
OTHER INFORMATION: EXPR
OTHER INFORMATION: EXPR
OTHER INFORMATION: EXP
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Best Local S
Matches 163
                                                                                                 CURRENT APPLICATION NUMBER: US/09/816,095
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09816095 Patent No. US20020137164A1
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEO ID NO 20174
                                                                                                                                                                                                      TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PITLE OF INVENTION: THERROF FILE REFERENCE: CL001147
                                      LENGTH: 99916
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                        APPLICANT: GAN, Weiniu
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                       FEATURE:
NAME/KEY: misc_feature
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hes 163;
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N: EXPRESSED IN LUNG, SIGNAL = 1.2

N: EXPRESSED IN HELA, SIGNAL = 1.4

N: EXPRESSED IN BRAIN, SIGNAL = 1.4

N: EXPRESSED IN HBL100, SIGNAL = 1.1

N: EXPRESSED IN PLACENTA, SIGNAL = 1.5

N: EXPRESSED IN PLACENTA, SIGNAL = 1.5

N: EXPRESSED IN HEART, SIGNAL = 1.5

N: EXPRESSED IN HEART, SIGNAL = 1.5

N: EXPRESSED IN HEART, SIGNAL = 1.5
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EXPRESSED IN BT474, SIGNAL = 1.5
EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
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US-09-771-208-20
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                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin version 3.0
SEQ ID NO 20
LENCTH: 659158
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/09771208 Patent No. US20020155564A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BRADFORD, ERIC
APPLICANT: HORVAT: SIMON
TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
FILE REFERENCE: 407T-923710US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/771,208
CURRENT FILING DATE: 2001-01-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MEDRANO, JUAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 20
                       NAME/KEY: misc_feature
LOCATION: (34686)..(346823)
OTHER INFORMATION: n is unidentified
NAME/KEY: misc_feature
LOCATION: (317174)..(317193)
OTHER INFORMATION: n is unidentified
                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (602465)..(602485)
OTHER INFORMATION: n is unidentified
NAME/KEY: misc_feature
LOCATION: (546998)..(547017)
OTHER INFORMATION: n is unidentified
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                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (123459)..(123478)
OTHER INFORMATION: n is unidentified
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OTHER INFORMATION: n =
                                                                                                                              NAME/KEY: misc_feature
LOCATION: (390986)...(391005)
OTHER INFORMATION: n is unidentified
                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (494715)..(494814)
OTHER INFORMATION: n is unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mus musculus
                NAME/KEY:
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            feature
..(280373)
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Pred. No. 17;
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
LENGTH: 29544
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Best Local
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/464,767
CURRENT FILING DATE: 1999-12-16
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SOFTWARE: PatentIn version 3.0
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LOCATION: (132680)..(132700)
OTHER INFORMATION: n is unidentified
NAME/KEY: misc_feature
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LOCATION: (170625)..(170645)
OTHER INFORMATION: n is unidentified
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OTHER INFORMATION: n is unidentified
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OTHER INFORMATION: n is unidentified
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                                                                                                                                                                       TTGATTCAAGACCATGATTTTCACAAAACGTTGACCAGTATTTTTTAGCTACTGAAATTT 6646
                                                       TTACAAAACATTCTCTGTTTACCTCATAACCTATATCGGTAGCTATT 6753
                                                                                  GCCAATTGCCTCGTTCCATCACTTCTTCTACATCTTATAAACGATTTCCTCTCTCC
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Pred. No.
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Pred. No. 9.1;
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APPLICANT: Lok, Si
APPLICANT: Holloway,
TITLE OF INVENTION: Hu
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APPLICANT: Both, Gerald
APPLICANT: Boyle, David
APPLICANT: Vrati, Sudhanshu
TITLE OF INVENTION: DNA Encoding Ovine Adenovirus (OAV287)
FILE REFERENCE: 50179-073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENCTH: 32745
TYPE: DNA
                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09947971 Patent No. US20020143148A1
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Best Local Similarity 50.9%;
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CURRENT FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 3
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CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 00-83
                                                                                                 NAME/KEY: misc_feature
LOCATION: 318, 333, 339,
LOCATION: 390, 393, 396,
LOCATION: 480, 486, 492,
                                                                                                                                                       LOCATION: 177, 186, 189, 201, LOCATION: 177, 186, 189, 201, 107HER INFORMATION: 246, 252, 255, 261,
                                                                                                                                                                                                                   OTHER INFORMATION: This degenerate nucleotide sequence OTHER INFORMATION: amino acid sequence of SEQ ID NO:2. NAME/KEY: misc_feature
                                                                                                                                                                                         LOCATION: 3, 9, 1;
LOCATION: 84, 87,
                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                 NAME/KEY: misc_feature LOCATION: 597, 606, 60
                                                                          LOCATION: 537, 540, 5
                                                                                                                                                    OTHER INFORMATION: n = A,T,C or
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1, 117, 141, 1
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US-09-933-797-413/c
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                                                                                                        Matches
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                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-05-14
NUMBER OF SEQ ID NOS: 811
                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/933,797 CURRENT FILING DATE: 2001-08-22
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/09/482,933 PRIOR FILING DATE: 2000-01-14
                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1999-05/14
                                                                                                                                                                                                                                                                                                                                                  PRIOR
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LOCATION: 843, 852, 855, 861, 864,
LOCATION: 903, 906, 909, 921, 924,
OTHER INFORMATION: n = A,T,C or G
                                    182
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                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US99/10746
TACAGAGGAAGCTTCTCGCTATCGACGCCATCGAAGCTTCCTACAATTTCTCCCCGTTC 133
                                                                TTTTTATTTTTTTTTTCAGTAAAAGAAATGTCATCGTCAAATTGGATCGACGACGCTTT 73
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                                  TCTCTTTTGTGCTTTTGAAATCCGAGGTGGMTGATTCTCAAGTACCAAGTTTGAAATGTT 123
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23.2%; Pred.
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                                                                                                    Score 34.6; DE Pred. No. 1.2; 1; Mismatches
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Pred. No.
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 5350
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                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2001-01-29
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PRIOR APPLICATION NUMBER: PCT/US01/0067
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
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OTHER INFORMATION: MAP TO ACO00053.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL =
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL =
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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Chen, Wensheng
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; OTHER INFORMATION: EXPRESSED US-09-864-761-5350
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APPLICANT: WEBSTER, Marion et al.
APPLICANT: WEBSTER, Marion et al.
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001193
                                                                                                                                                                                                Sequence 6599, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
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                               APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-x7
FILE REFERENCE: Acomica-x7
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 5
   PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
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LOCATION: (1) ...(53226)
OTHER INFORMATION: n =
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Sequence 8066, Application Patent No. US20020048763A1
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Best Local
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.4

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
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APPLICATION NUMBER: PCT/US01/00670
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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CURRENT FILING DATE: 2001-05-23
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OTHER INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO
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APPLICATION NUMBER: PCT/US01/00669
APPLICATION DATE: 2001-01-30
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IN HEART, SIGNAL = 3.3
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Pred. No. 2.
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US-09-925-302-270
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US-09-925-302-270/c
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US-09-864-761-8619
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CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
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                                        PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT
                                                                                     PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                  PRIOR APPLICATION NUMBER: GB 24263.6
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Local Similarity 56.1%;
APPLICATION NUMBER: PCT/US01/00664
                       FILING DATE:
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Hanzel, David K.
Chen, Wensheng
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine
SEQ ID NO 8619
LENGTH: 556
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OTHER INFORMATION: MAP TO AC023000.2

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9

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Search completed: November
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Matches 107
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PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                     GATGATGATGATGGTGATAATGATATTGATAATGGTGGGGGCGATG
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Post-processing: Minimum Match 0%
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US-08-232-463-14
US-09-300-672-3
US-08-485-216-1
US-08-485-252-11
US-08-485-352-1
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US-09-346-408-3
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US-09-134-001C-762
US-09-134-001C-2258
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US-09-416-213-1
US-09-315-676-1
US-09-323-676-1
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US-08-961-527-111
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Sequence 70, Appl Sequence 5, Appli Sequence 5, Appli Sequence 205, Appli Sequence 207, Appli Sequence 10, Appli Sequence 1, Appli Sequence 762, Appli Sequence 175, Appli Sequence 1, Appli Seq
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similarity 72; Conserv	-70 . Application US 6090620 FORMATION: T: Fu, Ying-Hui T: Yu, Chang-En T: Oshima, Junk Mulligan, Jo T: Schellenberg INVENTION: GEN INVENTION: GEN INVENTION: WER F SEQUENCES: 20 NDENCE ADDRESS: SEE: SEED and B : 6300 Columbia Seattle Washington Y: USA 98104-7092 READABLE FORM: TYPE: Floppy d ER: IBM PC comp ING SYSTEM: PC- RE: Patentin Re APPLICATION DATA ATION NUMBER: NO. 6090620tenb RATION NUMBER: NO. 6090620tenb RATION NUMBER: NO. 6090620tenb RATION UNGBER: NO. 6090620tenb		. 0 0 1 1		
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Score 111; Pred. No. 0; Mismatc	/08781891 o	AL	US-08- US-08- US-09- US-09-	US-09- US-09- US-09- PCT-US-09- US-09-	US-08-781-891-208 US-08-559-896B-1 US-08-765-332-140 US-09-448-894-140 US-09-448-894-140 US-07-876-280-8 US-08-049-783-5 US-08-316-301A-9
e 111; . No. ismatc		ALIGNMENTS	- 420-9 - 370-9 - 370-9 - 023-0 - 334-2	-904-2 -076-1 -222-5 -222-03 S92-03 -149-4	-781 -8 -559 -8 -765 -3 -765 -3 -448 -8 -876 -2 -049 -7
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Sequence 11, Application US/09791211

Patent NO. 6448080

GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
FILE REFERENCE: RTS-0205
CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 11
SEQ ID NO 11
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 272; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens FEATURE:
573 CTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGATGGTGACTCTGTGAAG
                                                                                                             493 TTATACAATAGAGGGAAACT---TGGCAAAGTTGCACTAATTCAGTTGTGTTTTCTGAG
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                                                                  AATTATTGTGATGTTATGCATATTTTT---CATTCTGGTATCCCTCAAAGTCTCCAACAT
                                                                                                                                    AGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGACTGTCCAGATATGTGTAGATAGT
                                                                                                                                                                                       GATATTAGCATGAGTCTATCAGATGGGGATGTGGTGGGATTTGACATGGAGTGGCCACCA
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                                       AGCAAATGTTACTTGCTTCCACGTTTCTTCCATGTCAGTTTTTCCCCAGGGATTAAAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAAGAGCTCCTGAAGCCAAACAGAATCAGGCTTGGGAACTGGGAGTTTTATCCTCTGTCA
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                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                             10.6%;
                                                                                                                                                                                                                                                             Score 111; DB 4; Length 5208; Pred. No. 2.5e-25; 0; Mismatches 225; Indels
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                                       609
                                                                                                             549
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Massachusetts Institute for Technology
APPLICANT: Leonard P. Guarente
APPLICANT: Leonard P. Guarente
TITLE OF INVENTION: ASSAYS FOR COMPOUNDS WHICH EXTEND LIFE
TITLE OF INVENTION: SPAN
FILE REFERENCE: MIT-7720PA
CURRENT APPLICATION NUMBER: US/09/127,670
CURRENT FILING DATE: 1998-07-31
EARLIER APPLICATION NUMBER: US 60/054,629
EARLIER APPLICATION NUMBER: US 60/054,629
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 6476
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; LOCATION: (229)...(4432)
US-09-127-670-5
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US-09-127-670-5
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                                                                                                                                                                                                                                                                                                                                                                 Matches 199;
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Murine
FEATURE:
                     718
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                                                                                                                                                                                                                                                                                        494 GCAGAGTCGCAGTGATCCAGTTGTGTGTGTCTGAGAACAAATGTTACTTGTTTCACATTT 553
                                                                                                                                                                                                                                                                                                                         481 GGAAGGTTGCGACTGTCCAGATATGTGTAGATAGTAATTATTGTGATGTTATGCATATTT 540
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                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                              TT---CATTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAA 597
GGGGCCTTGCCTCACCTGAGAGACACTTGTTTGCAAAGAGCTCCTGAAGCCAAACAGAA
                                                           TGGAGAGTTTTGTGGAGCTGACGGATGTTGCCAATGAAAAGTTGAAGTGCGCAGAGACCT
                                                                                            TCAAAGATGTTGAGGATCTTTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAAAAAAT
                                                                                                                                                                                                               CTTCCATGTCAGTTTTCCCCCCAGGGATTAAAAAATGTTACTAGAAAAACAAATCAATTAAGA
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                                                                                                                                    AGGCAGGGGTTGGGATTGAAGGGGGACCAGTGGAAACTTCTGCGTGATTTTGACGTCAAGT 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAACAGCTCCTGAAAGACAAGTCTATCCGCTGTAGCAATTGGAGTAAATTTCCTCTCACT
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                                                                                                                                                                                                                                                                                                                                                                                7.9%;
                                                                                                                                                                                                                                                                                                                                                             Score 82.8; DB 4;
Pred. No. 3.7e-16;
0; Mismatches 172;
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; LOCATION:
US-08-781-891-205
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US-08-781-891-205
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Best Local Similarity
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                                                                                                                                                                                                                  Matches 179;
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                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 205:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
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                                     630
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   562
                                                                                       570 CATCTTATTGAAGATTCAACACTTGTAAAGGTAGGTAGTTGGAATTGATGGTGACTCTGTG 629
                                                                                                                                                                             510 GATAGTAATTATTGTGATGTTATGCATATTTTTCATTCTGGTATCCCTCAAAGTCTCCAA 569
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                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 4792 base pairs
                               AAGCTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGCC 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGATGCTTATGCT 867
AAACTTCTGCGTGATTTTGACGTCAAGTTGGAGAGTTTTGTGGAGCTGACGGATGTTGCC
                                                                   ATGTTACTAGAAAACAAATCAATTAAGAAGGCAGGGGTTGGGATTGAAGGGGACCAGTGG
                                                                                                                                         GAGAGCAAATGTTACTTGTTTCACATTTCTTCCATGTCAGTTTTCCCCCCAGGGATTAAAA 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCGCTGCAGCAATTGGAGTAATTTCCCCCCTCACTGAGGACCAGAAACTGTATGCAGCCA 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08781891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                        CDS
145..4347
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                                                                                                                                                                                                                Score 81.2; DB 3;
Pred. No. 1e-15;
0; Mismatches 163;
                                                                                                                                                                                                                                                  DB 3; Length 4792;
                                                                                                                                                                                                                Indels
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SEQ ID NO 10
LENGTH: 98844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Patent No. 6448080
                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE:
                                                                                                                                          45421 TACAGTTTTTCCCCCAGGGATTAAAAATGTTGCTTGAAAATAAAGCAGTTAAAAAAGGCAGG
                                                                      45481
                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 87130 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure
LOCATION: 65471
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: unknown
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                          LOCATION: 89049
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
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                                                                                                                                                              545 TTCTGGTATCCCTCAAAGTCTCCAACATCTTATTGAAGATTCAACACTTGTAAAGGTAGG 604
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                                                                      TGTAGGAATTGAAGGAGATCAGTGGAAACTTCTACGTGACTTTGATATCAAATTGAAGAA 45540
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TTTTGTGGAGTTGACAGATGTTGCCAATAAAAA 45573
                                                                                                      TATTGGAATTGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAAGA 664
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                                                                                                                                                                                                                                   Similarity
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Pred. No. 1.4e
0; Mismatches
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l.4e-06;
nes 61;
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US-08-232-463-14
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US-08-781-891-207
                                                                                                             Sequence 14, Application US/08232463 Patent No. 5670367
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Best Local Similarity 56.5%;
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                                                                         GENERAL INFORMATION:
APPLICANT: DORNER
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APPLICANT: Fu, Yi
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                                                                                                                                                                                                                               19909
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: NO. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
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                   APPLICANT: SCHEIFL APPLICANT: FALKNER TITLE OF INVENTION:
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APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
     NUMBER
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                                                                                                                                                                                                                                                                  665
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FALKNER, F. G.
NVENTION: RECOMBINANT FOWLPOX VIRUS
SEQUENCES: 52
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                                                     SCHEIFLINGER, F.
                                                                         DORNER, F.
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206) 682-6031
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RESULT 8
US-09-300-672-3
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US-08-232-463-14
GENERAL INFORMATION:
APPLICANT: Finkelstein, Ruth R
APPLICANT: Lynch, Tim
                                             Sequence 3, Application US/09300672 Patent No. 6248937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)683-4109
                                                                                                                                                 1052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                        9 ATTAATTTTATTTTTTGTTTCAGTAAAAGAAATGTCATCGTCAAATTGGATCGACGAC 68
                                                                                                                                                                                                                                                                                                            CGTTCTTCTTCTTCTTCCTCCTCTGCTGCTCCGACCGTACAAGCTACAACCTCCGTCCAT 188
                                                                                                                                                                               ATCACTTCTTCTACATCTTATAAACGATTTCCTCTCTCCCGTTGCC 294
                                                                                                                                                                                                              GGCCACGAGGAGGATCCAAATCAAATCCCCCAATAATATCCGTCGCCAATTGCCTCGTTCC 248
                                                                                                                                                                                                                                                                                                                                            GCTTTTACAGAGGAAGAGCTTCTCGCTATCGACGCCATCGAAGCTTCCTACAATTTCTCC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 4.7%; Score 49.2; DB 1; Similarity 11.5%; Pred. No. 2.8e-05; 33; Conservative 140; Mismatches 113
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APPLICANT:

Goodman, Howard M.

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; LOCATION: (151)..(1134)
US-09-300-672-1
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Goodman, Howard M.
APPLICANT: Wang, Ming-Li
TITLE OF INVENTION: A TRANSCRIPTION FACTOR REGULATING
TITLE OF INVENTION: QUALITY AND COLD-TOLERANCE
TITLE OF INVENTION: QUALITY AND COLD-TOLERANCE
FILE REFERENCE: 480.89(HY)
CURRENT FAPPLICATION NUMBER: US/09/300,672
CURRENT FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1499
TYPE: DNA
ORGANISM: Arabidopsis
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Best Local Similarity
Matches 83; Conserv
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CURRENT FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 1500
                                                                                                                                                                          172 CTACAACCTCCGTCCATGGCCACGAGGAGGATCCAAATCAAATCCCCCAATAATATCCGTC 231
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                                                         224 CTCAATCCGATTCCACCACCGACTCATCAACTTCCT 259
                                                                                               232 GCCAATTGCCTCGTTCCATCACTTCTTCTACATCTT 267
                                                                                                                                                                                                                    104 CTCTCTACTTCCTCTTCCTTCTTCTTCTTCTTCTTCATCTATGGACCCTTTAG 163
                                                                                                                                                                                                                                                            112 CTTCCTACAATTTCTCCCGTTCTTCTTCTTCTTCTTCCTGCTGCTGCTCCGACCGTACAAG 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 CTTCCCAACATCAACACCATCTGGAAGATAATAACCAAACCCTAACCCATAATAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 CTACAACCTCCGTCCATGGCCACGAGGAGGATCCAAATCAAATCCCCCAATAATATCCGTC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity hes 83; Conserv
                                                                                                                                        CTTCCCAACATCAACCAACCATCTGGAAGATAATAACCAAACCCTAACCCATAATAATC
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                        3.7%;
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                                                                                                                                                                                                                                                                                                   Score 39.2; DB 4; Length 1500; Pred. No. 0.017; O; Mismatches 73; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39.2; DB Pred. No. 0.017;
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                                                                                                                                                                                                                                                                                                     0;
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; ORIGINAL SOURCE:
; ORGANISM: Plasmodium yoelii
US-08-929-329-1
                                                                                                                                                  В
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                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.5%;
Best Local Similarity 46.0%;
                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (317) 231-74 INFORMATION FOR SEQ ID NO:
3152
                                                                                                                                                                                                                                                                                                      2912 CATTAATATTCCTTGTTTTCTTGTTTTAGAATATATGTTCATAATGTATCCTTCTGT 2971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-7745
TELEPHONE: (317) 231-7433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,329
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APPLICANT: Kappe, Stefan
TITLE OF INVENTION: Plasmodium Proteins U
TITLE OF INVENTION: Vaccine Compositions
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                               494 TGTCCAGATATGTGTAGATAGTAATTATTGTGATGTTATGCATATTTTTCATTCTGGTAT 553
                                                                                                                                                                                                                                                                                                                                        434 CTTGGATATTGAGTGGAGACCAAGTTTTAGAAAAGGTGTTCTCCCGGGGAAGGTTGCGAC 493
                                   674 TCTTTCAGATTTAGCCAACCAAAAAATTGGTGGA 707
                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
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TAATCAAAATATTAATCTCGTAAAACTTGATGAA 3185
                                                                                                        TGATGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGA 673
                                                                                                                                                  TTCGAGTAATTTGTATAATGCTAAAAGGAGAATGTTATTATATAAATGAAAAACCTAATTG
                                                                         TGTTATTGACAAAGTAAAATCATTTCTCATTTACTTCCCTCACAACAAATGATATTGATTT 3151
                                                                                                                                                                                                                           TTTACAGAGAACTGAAAAAAAAATTATTGGGGTGTGTGGGTTGCAAGTGAATCTGTTAA 3031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5433 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       double
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RESULT 11 US-08-485-216-1

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                                                                                RESULT 12
US-09-003-245-1
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LOCATION:
US-08-485-216-1
               Sequence 1, Application US/09003245
Patent No. 5901189
GENERAL INFORMATION:
APPLICANT: Chan, Voon L.
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Mueller, Douglas P.
REGISTRATION NUMBER: 30,300
REFERENCE/DOCKET NUMBER: 79:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612,332-5300
     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: WO 9. FILING DATE: 13-MAY-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chan, Voon Loong
APPLICANT: Hani, Eric K.
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                                                                                                                                                                                                                                                                                                                                          798
                                                                                                                                                                             689 CAACCAAAAATTGGTGGAGATAAAAA 715
                                                                                                                                                                                                                                                                                                             569
                                                                                                                                                                                                                                                                                                                                                                        509 AGATAGTAATTATTGTGATGTTATGCATATTTTTCATTCTGGTATCCCTCAAAGTCTCCA 568
                                                                                                                                                                                                             918 TAATATCATTCCAGATATTGTAACGATTAAAATGAGTGTTAGAGGATTAGATAATGAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/485,216 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
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                                                                                                                                               TAGAAAGCTAACTGAAGAAAAAAAAA 1004
                                                                                                                                                                                                                                                                                                ACATCTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGATTGGTGATGGTGACTCTGT
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                                                                                                                                                                                                                                          GAAGCTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGC
                                                                                                                                                                                                                                                                                                                                                                                                          99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H: 1338 base pairs
nucleic acid
NDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                        similarity 47.8
99; Conservative
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3100 No. 5695960west Center,
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Chan, Voon
Hani, Eric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                         3.3%;
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 <u>ج</u> :
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                                                                                                                                                                                                                                        Query Match
Best Local Similarity 47.8
---- 99; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  CLONE: PHIFTO POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1338 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
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ORIGINAL SOURCE:
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                    689 CAACCAAAAAATTGGTGGAGATAAAAA 715
978 TAGAAAGCTAACTGAAGAAAAAAAAA 1004
                                                               918 TAATATCATTCCAGATATTGTAACGATTAAAATGAGTGTTAGAGGATTAGATAATGAAAC
                                                                                            629 GAAGCTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCTTTCAGATTTAGC 688
                                                                                                                             858 TGTTGATCCCCAAAATTCAGCAGTTGTAAGCATAGGAGCTTTTAATGCTGGACATGCTTT 917
                                                                                                                                              569 ACATCTTATTGAAGATTCAACACTTGTAAAGGTAGGTATTGGAATTGGATGGTGACTCTGT 628
                                                                                                                                                                                        798 AGATCCTATTTATGCTGCTTCTTTACTTATTGTAACTTTACAAAGCATAGTATCTTGCAA 857
                                                                                                                                                                                                              509 AGATAGTAATTGTGATGTTATGCATATTTTTCATTCTGGTATCCCTCAAAGTCTCCA 568
                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         יייטאאוSM: Campylobacter jejuni
STRAIN: TGH9011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Mueller, Douglas REGISTRATION NUMBER: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 06-JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Minneapolis STATE: Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY:
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Pred. No. 0.67;
0; Mismatches 108;
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RESULT 13 US-08-853-552-1

Sequence 1, Application US/08853552
Patent No. 6013501
GENERAL INFORMATION:
APPLICANT: Chan, Voon Loong

NUMBER OF SEQUENCES: 2

Eric K.

CORRESPONDENCE ADDRESS: APPLICANT: Hani, EX

ADDRESSEE:

Merchant & Gould

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US-09-346-408-3/c
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US-08-853-552-1
                                                                                                                                       Sequence 3, Application US/09346408B Patent No. 6338966
                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 99; Conserv
APPLICANT: Allen, Steve
APPLICANT: Anderson, Shawn
APPLICANT: Falco, Carl
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Genes Encoding Sulfate Assimilation
FILE REFERENCE: BB-1167-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 612/332-9081 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 612/332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    798
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                                                                                                                                                                                                                                                                                   689 CAACCAAAAATTGGTGGAGATAAAAA 715
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REFERENCE/DOCKET NUMBER: 7933.29US02
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OPERATING SYSTEM: PC-DOS/MS-DOS
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-762
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US-09-134-001C-762/c
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SEQ ID NO 3
LENGTH: 2280
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Best Local Similarity
Matches 111; Conserv
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LENGTH: 1272
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Momordica charantia
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                                                                                                                                                        198
                                                                                                                                                                                            617
                                                                                                                                                                                                                                                                                                                                                503 ATGTGTAGATAGTAATTATTGTGATGTTATGCATATTTTTCATTCTGGTATCCCTCAAAG 562
                                                                            138
                                                                                                                                                                                                                                  258
                                                                                                                                                                                                                                                                      563 TCTCCAACATCTTATTGAAGATTCAACACTTGTAAAGGTAG-----GTATTGGAATTGA 616
                                                                                                                                                                                                                                                                                                            318 AAGTCCAGGTAATACTTTAGTAGATATTTCTTGTCCACGTAATCCAGTTACCACTAATAT 259
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                                                                                                                TTCAGATTTAGCCAACCAAAAAATTGGTGGAGATAAAAA 715
                                                                                                                                                      AAAACTAGCATAAAATTGTGCAGTAAACACTGCAGTTTGAGTCAGAAATGCTGGACCAAT 139
                                                                                                                                                                                          TGGTGACTCTGTGAAGCTTTTCCATGACTATGGAGTTAGTATCAAAGATGTTGAGGATCT 676
                                                                                                                                                                                                                                  TCTCCAAATATTTATTTGAGCGCCTATATCTATAATAATAGAAATTAATATTGCAAATGC 199
                                                                            AGCTGATGTAGCCATTAAAAAAACTGAACCATATAATAA
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Pred. No. 0.
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Minimum DB
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Listing first 45 summaries
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Perfect score:
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Match Length
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Gapop 10.0 , Gapext 0.5
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1491
    98.4
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                                                                                                                                                                                                                                                                                                                                                                                                                       sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                  sp_phage:*
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                                                                                                                                                                                                                                                                                                                                                                                          sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                      sp_human:*
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sp_archeap:* .
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sp_virus:*
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sp_rvirus:*
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                                                                                                                                                                                                           SUMMARIES
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Q9ft68 arabidopsis
Q95vm6 arabidopsis
Q93530 xenopus lae
Q9z241 mus musculu
Q9jkd4 mus musculu
Q35v9 oryza sativ
Q9ve86 drosophila
Q9vef1 drosophila
Q9vef7 drosophila
Q9vef8 arabidopsis
Q93vs2 oryza sativ
Q9c216 neurospora
Q22964 arabidopsis
Q91k79 arabidopsis
Q91k79 arabidopsis
                                                                                                                                                                           Description
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92	92.5	92.5	93	93	93	94.5	94.5	95	95	95	96.5	97	97	97.5	98.5	98.5	101	102.5	103	105	110	111	111	•	112.5		127.5	142
6.2	6.2	6.2	6.2	6.2	6.2	6.3	6.3	6.4	6.4	6.4	6.5	6.5	6.5	6.5	6.6	6.6	6.8	6.9	6.9	7.0	7.4	7.4	7.4	7.5	7.5	8.1	8.6	9.5
237	1097	721	2224	552	488	416	353	4589	925	455	488	906	579	445	532	265	876	710	220	625	238	300	242	210	217	505	239	599
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Q9ZV70	013592	Q94B18	043737	Q9LVM8	Q9HJ76	096144	Q9LHG4	076506	Q9GUG1	Q9ZWS2	Q97JZ0	Q17281	Q9RQK2	O9YDVO	Q976Y3	Q9LHG5	Q17951	Q9NA69	Q9LHG1	Q9VIF1	Q9C7A5	Q9AL74	Q9LHG2	Q9LHG3	080886	Q9FIN8	Q9SIH3	Q96NP1
			•				•				**					-						-						
Q9zv70 arabidopsis	013592 saccharomyc	Q94b18 capsicum an	043737 homo sapien	Q91vm8 arabidopsis	Q9hj76 thermoplasm		4	076506 tetrahymena	a	Q9zws2 vigna mungo	0	Q17281 botryllus s	acillus st	Q9ydv0 aeropyrum p		Q91hg5 arabidopsis	Q17951 caenorhabdi	0	-	Q.	Q9c7a5 arabidopsis	a				Q9fin8 arabidopsis	arab	Q96np1 homo sapien

ALIGNMENTS

Qy 61 NIRROLPRSITSSTSYKRFPLSRCRARNFPAMREGGRILYSKTATEVDKRAMQLIKVLDT 120	MSSSNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSAAPTVQATTSVHGHEEDPNQIPN 60	Query Match 98.4%; Score 1466.5; DB 10; Length 285; Best Local Similarity 99.0%; Pred. No. 1.2e-126; Matches 285; Conservative 0; Mismatches 0; Indels 3; Gaps 1;	SQ SEQUENCE 285 AA; 31750 MW; A198CB93653E229B CRC64;	 RL Nucleic Acids Res. 21:4275-4282(2000). DR EMBL; AJ404476; CAC14871.1; -	RT "Molecular characterisation of RecQ homologues in Arabidopsis	 RP SEQUENCE FROM N.A.	OC eurosids 11; Brassicales; Brassicaceae; Arabidopsis.		GN WRNEXO.	01-DEC-2001 (TrEMBLrel. 19, Last	01-MAR-2001 (TrEMBLrel. 16,	01-MAR-2001 (TrEMBLrel.	ID 09FT68 PRELIMINARY: PRT: 285 AA.	RESULT 1

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C Q9SYM6;
T Q1-MAY-2000 (TrEMBLrel. 13, Created)
T Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
T Q1-MAY-2001 (TrEMBLrel. 17, Last annotation update)
T Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
E HYPOTHETICAL 35 1 KDA PROTEIN.
N F18A5.260 OR AT4G13870.
N F18A5.260 OR AT4G13870.
E Lukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
C Spermatophyta; Magnollophyta; eudicotyledons; core eudicences annotation of the streptophyta; Tr
C Spermatophyta; Magnollophyta; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AL035528; CAB36651.1; -
EMBL; AL161537; CAB78429.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Bevan M., Weber N., Grueninger D., Schmidheini
Mewes H.W., Mayer K.F.X., Lemcke K., Schweller
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002562; 3_5_exonuclease, Pfam; PF01612; 3_5_exonuclease; 1. SMART; SM00474; 35EXOC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical pr
SEQUENCE 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EU Arabidopsis sequencing project; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ
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LKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKV--
                                                                   DSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKEL
                                                                                                                                                                KRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLIE
                                                                                                                                                                                                                                                            NIRRQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDT
                                              DSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKEL
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95.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1439.5; DB Pred. No. 4e-124; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 448D7ACC375D4D22 CRC64;
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edons; core eudicots; Rosic
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Best Local S
Matches 82
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Interpro: IPR00150; I
Interpro: IPR002121; I
Interpro: IPR002121; Pfam; PF01612; 3_5_ex; Pfam; PF00270; DEAD;
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SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                   SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
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-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)

-i- SIMILARITY: BELONGS TO THE RECQ SUBFAMILY OF

-i- SIMILARITY: CONTAINS 1 HRDC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "FFA-1, a protein that promotes the formation within nuclei.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND FUNCTION. MEDLINE-98301165; PubMed-98597700; Yan H., Chen C.-Y., Kobayashi R., Ne "Replication focus-forming activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NCT-2001 (TrEMBLrel. 18, Last annotation update)
werner Syndrome Helicase Homolog (FOCUS FORMING A
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                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                  нydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yan H., Newport J
"FFA-1, a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96032793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION
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Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FFA-1
                                                                                                                                                                                                                                                                                                                                           NIAMOC
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ence 269:1883-1885(1995).

FUNCTION: ESSENTIAL FOR THE FORMATION OF DNA REPLICATION FOCA-
FUNCTION: ESSENTIAL FOR THE FORMATION OF DNA REPLICATION FOCA-
CENTERS; STABLY ASSOCIATES WITH FOCI ELEMENTS GENERATING BING
CENTERS; FOR RP-A. EXHIBITS A MAGNESIUM DEPENDENT ATP-DEPENDENT
SITES FOR RP-A. EXHIBITS A MAGNESIUM DEPENDENT ATP-DEPENDENT
SITES FOR RP-A. EXHIBITS A MAGNESIUM DEPENDENT ATP-DEPENDENT

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SITES FOR RP-A. EXHIBITS A MAGNESIUM DEPENDENT ATP-DEPENDENT

SITES FOR RP-A. EXHIBITS A MAGNESIUM DEPENDENT ATP-DEPENDENT

SITES FOR RP-A. EXHIBITS A MAGNESIUM DEPENDENT ATP-DEPENDENT

SITES FOR RP-A. EXHIBITS A MAGNESIUM DEPENDENT ATP-DEPENDENT

SITES FOR RP-A. EXHIBITS A MAGNESIUM DEPENDENT ATP-DEPENDENT

SITES FOR RP-A. EXHIBITS A MAGNESIUM DEPENDENT ATP-DEPENDENT ATP-DE
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                                                              KRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIF-
                                                                                                                      SLQRKLPEWMSVKQQEDRIDDAKKSFCKKNILEDNLPFMKFNGSIVYSYESNDCSLLSED
HSGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWG
                                         IRSSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00271; helicase_C; PF00570; HRDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                   SM00487;
SM00490;
SM00341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00474;
                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                 461
1098
512
609
1436
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                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus
                                                                                                                                                                                                                                                                                                                                                              icase; ATP-binding; DNA-binding; 1 467 POLY-ASP.
                                                                                                                                                                                                                                                                                                                                                                                                                 DEXDC; 1.
                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                   HRDC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           35EXOc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC63512.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _5_exonuclease;
                                                                                                                                                                                                                                                                                                    467
1117
519
612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=7569932;
                                       EEDV - - LGFDIEWPPVYTKG - KTGKVALIQVCVSEKKCYLFHISP
                                                                                                                                                                                                                       22.8%;
35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HRDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicase_C.
                                                                                                                                                                                                                                                                                   161850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5_exonuclease
                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                   W.
                                                                                                                                                                                                  Score 339.5; DB 13
Pred. No. 4.2e-22;
3; Mismatches 84;
                                                                                                                                                                                                                                                                                                                  HRDC.
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                      DEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FOCUS FORMING ACT
                                                                                                                                                                                                                                                                                 1BOX.
1BEAF05A25B4E230
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ty 1 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J.;
the
                                                                                                                                                                                                                                          DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Werner
                                                                                                                                                                                                                                                                                                                                                                                  Nuclear
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                                                                                                                        62
                                                                                                                                                             108
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RESULT
Q9JXD4
ID Q9
AC Q9
AC Q9
DT 01
DT 01
DT 01
DT WI
CON WI
CON M
OS M
OS M
OS EN
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Q9Z241
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Best Local S
Matches 74
                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF091216; AAC72359.1; -...

InterPro; IPR002562; 3_5_exonuclease
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
Pfam; PF001512; 3_5_exonuclease; 1.
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; helicase_C; 1.
SMART; SM00497; DEXDC; 1.
SMART; SM00497; DEXDC; 1.
SMART; SM00490; HELICC; 1.
ATP-binding; Helicase.
                                 Q9JKD4;
Q9JKD4;
01-OCT-2000
01-OCT-2000
01-DEC-2001
WRN PROTEIN.
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01-MAY-1999
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9Z241;
Q9Z241;
  Mus musculus (Mouse) 
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paeper B.W., Gayle M., Brady W., Swartz A Mulligan J., Galas D., Fu Y.-H.; "Genomic structure of the human Werner's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homolog.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                   VSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQY
                                                                                                                                                                                                                                               K---VATYQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYG
                                                                                                                                                                                                                                                                                          NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
                                                                                                                                              AATDAYAGLIIYQKLGNLGDTV
                                                                                                                                                                   AATDAYASWHLYKVLKDLPDAV
                                                                                                                                                                                       VKLESFVELTDVANEKLKCAETWSLNGLVKHVLGKQLLKDKSIRCSNWSNFPLTEDQKLY
                                                                                                                                                                                                                                  KRSRVAVIQLCVSENKCYLFHISSMSVFPQGLKMLLENKSIKKAGVGIEGDQWKLLRDFD
                                                                                                                                                                                                                                                                              NLPFLEFPGSIVYSYEASD----CSFLSEDISMRLSDGDV--VGFDMEWPPIYK----PG
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                                                                                                                                                                                                                                                                                                                                      Similarity
                                           (TrEMBLrel.) (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                      988
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                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                      AA;
 Chordata;
                                                                                                                                                                                                                                                                                                                                                                      111513 MW;
                                                                                                                                                                                                                                                                                                                                     22.7%;
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DEAD.
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19,
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10,
                                                                                                                                                                                                                                                                                                                           42;
                                           Created)
Last sequence Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                        Score 339; DB 11;
Pred. No. 2.8e-22;
2; Mismatches 72;
 Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                      DBD4D77FA55D5B2D CRC64;
                                           sequence update) annotation updat
                                                                                        1401
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  Vertebrata;
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                                           update)
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                                                                                                                                                                                                                                                                                                                                             Length 988;
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  Euteleostomi;
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Murinae; Mus
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                 035948 PRELIMINAKI,
035948;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TREMBLES SYNDROME PROTEIN.
SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00271; helicase_C; 1.
SMART; SM00474; 35EXOC; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
SMART; SM00341; HRDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                 Submitted (APR-1997)
                                                                                                          Wu J., He J., Mountz "mouse WRN.";
                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Mutations in the WRN Gene in Mice Accelerate Background.";
Mol. Cell. Biol. 20:3286-3291(2000).
EMBL; AF241636; AAF64490.1; -.
InterPro; IPR002562; 3_5_exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-20221574; PubMed-10757812;

Lombard D.B., Beard C., Johnson B., Me

Bronson R., Buhlmann J.E., Lipman R.,
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                  WRN OR WRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding; Helicase. SEQUENCE 1401 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002121; Pfam; PF00270; DEAD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLPFLEFPGSIVYSYEASD----CSFLSEDISMRLSDGDV--VGFDMEWPPIYK----PG
                                                                                                                                                                                                                                                                                                                                              AATDAYASWHLYKVLKDLPDAV
                                                                                                                                                                                                                                                                                                                                                                    VKLESFVELTDVANEKLKCAETWSLNGLVKHVLGKQLLKDKSIRCSNWSNFPLTEDQKLY
                                                                                                                                                                                                                                                                                                                                                                                        VSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQY
                                                                                                                                                                                                                                                                                                                                                                                                               KRSRVAVIQLCVSENKCYLFHISSMSVFPQGLKMLLENKSIKKAGVGIEGDQWKLLRDFD
          SM00474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity 36.6
74; Conservative
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35EXOc;
HELICc;
                                                                                                                                                                Rodentia;
                                                                                                                                                                            Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRDC.
                                                                3_5_exonuclease
                                                                                                                     J.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42;
                                                                                                EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                              285
                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rodentia; Sciurognathi; Muridae;
                                                     Score 339; DB 11;
Pred. No. 4.5e-22;
2; Mismatches 72;
                                                                                                              6CBC330CD072C670 CRC64;
                                                                                                                                                                                                                                                                                                                                                  Marciniak R.A., Dau
                                                                                                                                                                                                                                                                                                                           Mortality in a p53-Null
                                                                              Length 1401;
                                                      Indels
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86
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RESULTATION OF THE PROPERTY OF
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Best Local
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Best Local
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01-DEC-2001 (TremBLrel. 19, Created)

01-DEC-2001 (TremBLrel. 19, Last sequence up

01-DEC-2001 (TremBLrel. 19, Last annotation

P04E7H02.22 PROTEIN (P0682B08.3 PROTEIN).

P04E7H02.22 OR P0682B08.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spexmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0487H02.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q93VU9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP-binding; Helicase.
SEQUENCE 643 AA; 72821 MW;
268
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone: P0682B08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sasaki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                      128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
                                                                                                                                                                                                      152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116
                                                                                                                                                       8
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                                                                                                                                                                                                                                                                                                      92 MRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPGKVAT 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NIRRQLP-----RSITSSTSYKREPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
     AYASWHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQICVDSNYCDVMHIFHSG-IPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVE
                                                                                                DLSDLANQK----IGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAATD
                                                                                                                                                                                                                                                       VRFGSATIDTTVTSDVAAADEWARGVRAAARGGRGL-IVGLDCEWKPN-HVSWKTSKVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDISMRLSDGDV--VGFDMEWPPIYK----PGKRSRVAVIQLCVSENKCYLFHISSMSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVLDTKRDESGIAFVGLDIEWRPSFRKGVLPGK---VATVQICVDSNYCDVMHIFHSGI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLQRKFPEWMSMQSQRCATEEKACVQKNVLEDNLPFLEFPGSIVYSYEASD----CSFLS
                                                 DLEDACNRRLGLVGTGRRLGLKGYAREVLGMAMEKPRRVTMSNWEKRELDPAQVEYACID
                                                                                                                                                    LQLCAGERFCLVLQLFYANRVPPAVADLLGDPSVRLVGIGVGEDAAKLEADYGVWCAAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQGLKMLLENKSIKKAGVGIEGDQWKLLRDFDVKLESFVELTDVANEKLKCAETWSLNGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                   tted (MAY-2001) to the EMBL/GenBank/DDBJ databases
AP002883; BAB67862.1; -.
AP003578; BAB60933.1; -.
NCE 201 AA; 21899 MW; 85F35C0CC5386265 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (OCT-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsumoto T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                               16.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
                                                                                                                                                                                                                                                                                                                                                          36;
                                                                                                                                                                                                                                                                                                                                                                     Score 238; Ub ...
No. 6e-14;
                                                                                                                                                                                                                                                                                                                                                       Pred. No. 6e-:
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 330.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F9125C234ABBB757 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nes 83;
                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                       87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                       6;
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                                                 187
                                                                                                                                                 127
                                                                                                                                                                                                                                                    67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171
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QΥ

41 TVQATTSVHGHEEDPNQIPNNIRRQLPRSITSSTSYKREPLSRCRARNEPAMRFGGRILY

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RESULT
Q9VE86
                                                                                                                                           ACD CONTRACTOR OF CONTRACTOR CONT
                                                                                                                                                                                                                                                                                                     RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Bayenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Bayenport L.B., Davies P.,
RA Cherry J.M., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Colodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Sylrskas R., Tector C., Turner R., Venter E., Mang A.H., Wang A.H., Wang A.H., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yang S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yiliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yiliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yiliams G., Shong M., Scholl M., Shong G., Zhao Q., Zhang G., Zhao Q., Zhang G., Zhao Q., Zhang G., Zhao Q., Zhang S., Yao Q.A.,
RA Yiliams M. Shang M.G., Shang S., Shang G., Zhao Q., Zhang G., Zhao Q., Zhang G., Zhao Q., Zhao Q., Zhang G., Zhao Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
   Matches
                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                            Pfam; PF01612; 3_5_exon
SMART; SM00474; 35EXOc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9VE86
                                                                                                                                                                                                                                                                                      FlyBase; FBgn0038608; CG7670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ephydroidea;
                                                                                                                                                                                                                                                     InterPro; IPR002562; 3_5_exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 AYVSYKL
                                    Similarity
                                                                                                                                           346 AA;
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194
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                                                                                                                                                                                                                 _exonuclease;
                                                                                                                                               39398 MW;
                                 15.4%;
26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13,
13,
17,
43;
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Last sequence up
Last annotation
Score 229.5; DB 5;
Pred. No. 7.7e-13;
3; Mismatches 123;
                                                                                                                                           3150A9B4EFB74EB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₿
   Indels
                                                                     Length
13;
Gaps
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RESULT 10
Q9VGN7
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AC ID
                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q961E1;
Q961E1;
Q1-DEC-2001
Q1-DEC-2001
Q1-DEC-2001
Q9VGN7;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R. Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J. Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY051647; AAK93071.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musce Ephydroidea; Drosophilidae; Drosophila.
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                                                                                      308
                                                                                                                                            248
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                                                                                    YRELE 312
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YRELE 305
                                                                                                               YKVLK
                                                                                                                                           WCNEVCETGGRWSLERLTNFIAKKAMDKSKKVRMSKWHVIPLDENQLMYAAIDVYIGQVI
                                                                                                                                                                    LANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHL
                                                                                                                                                                                                   CYIYQLTNVKKLPAALVALINHPKVRLHGVNIKNDFRKLARDFPEVTAEPLIEKCVDLGL
                                                                                                                                                                                                                              CDVMHIFH-SGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDY-----GVSIKDVEDLSD
                                                                                                                                                                                                                                                          FTESQDIAASADDVLQWVEKQKAE--VVPMAFDMEWPFSFQTG--PGKSAVIQICVDEKC
                                                                                                                                                                                                                                                                                      SKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKVLK
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                                                                                                                                                                                                                                                                                                                    TPDVTEKLAMEEENP---PKRRSSRLTRSTRSMAEDGSPSPEKEKPEKLPFIKYKGAIKY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYIYQLTNVKKLPAALVALINHPKVRLHGVNIKNDFRKLARDFPEVTAEPLIEKCVDLGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTESQDIAASADDVLQWVEKQKDE--VVPMAFDMEWPFSFQTG--PGKSAVIQICVDEKC
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26.5%;
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19,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                         Score 221.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                             Mismatches 124;
            583 AA
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                                                                                                                                                                                                                                                                                                                                                                                                         DB 5;
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RA Adams N.D., Cenliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Cenliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Cenliker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.M., Basu A., Barter E.G., Helt G., Welson C.R., Maklos G.L.G.,
RA Man K.H., Doyle C., Bayter E.G., Helt G., Welson C.R., Maklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Baytaktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hortis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hortis N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Hortis N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Hostin D., Houston K.A., Homand T.J., Wei M.-H., Ibagwan C.,
RA Hortis N., May M., Murphy B., Murphy B., Murphy B., Merson D.I.,
RA Meinert K., Rennigton K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Meinert K., Rennigton K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Weisensch M., Shupski M.P., Sinth T.,
RA Shue B.C., Sideler Klamos I., Singpson M., Skupski M.P., Santh T.,
RA Shue J., Wei M.-H., Long S., Y
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Best Local
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01-MAR-2001 (Tri
01-DEC-2001 (Tri
01-DEC-2001 (Tri
CG6744 PROTEIN.
CG6744.
                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0037901; CG6744.
InterPro; IPR002562; 3_5_exonuclease
SMART; SM00474; 35EXOC; 1.
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NCBI_TaxID=7227;

[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
167
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                                                                                                            162
                                                                                                                                                                                     109
                                                                                                                                                71
                                                                                                                                                                                   KRAMQLIKVLDTKRDESGIAFVGLDIEW-----RPSFRKGVLPGKVATVQICVDSNYC
                                 GGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLY~KVLK
                                                                       ALFRICHMKQIPQDLRELLEDDSVIKVGVAPQEDAMKLSHDYGVGVASTLDLRFLC--VM
                                                                                                          DVMHIFH-SGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKI
                                                                                                                                                 KNHCQTFKVL------GFDCEWITVGGSRRP-----VALLQLSSHRGLC
AGHKPEGLGKLSKTHLNYTLDKHWRLACSNWEAKTLEPKQLDYAANDALMAVAIYQKLCR
                                                                                                                                                                                                                          61;
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1 (TrEMBLrel.
1 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                     583 AA;
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                     66866 MW;
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16,
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Last
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                                                                                                                                                                                                                                                Score 212.5;
Pred. No. 5.
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                                                                                                                                                                                                                                                              Length 583;
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Best I
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MEDLINE-21.016719; PubMed-11130712;
Mitco O., Alcasi H., Araujo R., Bownan C.L., Brooks S.Y.,
White O., Alcasi H., Araujo R., Bownan C.L., Brooks S.Y.,
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujil C.Y.,
Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Khan S., Khaykin E.,
Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
Hunter J.L., Jenkins J., Johnson-Hopson C., Kuan A., Lam B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09C7K6;
09C7K6;
01-JUN-2001
01-JUN-2001
01-CCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; "Sequence and analysis of chromosome l of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002562; 3_5_exonuc
Pfam; PF01612; 3_5_exonuclease;
SMART; SM00474; 35EXOC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 408:816-820(2000).
EMBL: AC069159; AAG50917.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryose; Spermatophyta; Magnollophyta; eudicotyledons; eurcsids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                            thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. COLUMBIA;
MEDLINE-21016719; PubMed-11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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 549
                                 281
                                                                  496
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                                                                                                                                                                                                                                                                                                       Match
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HPPHDSSS
                             LPDAVSGS 288
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                                                                G-----GLAGLTKKILGVSLNKTR--RNSDWEQRPLSQNQLEYAALDAAVLIHIFRHVRD
                                                                                                GGDKKWGLASLTETLYCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKYLKD
                                                                                                                                 SKSTLKLVSLTEDYPDHKLSSGYNFQCDIKQLALSYG-DLKCFERYDMLLDIQNVFNEPF
                                                                                                                                                                                                    GCRVVGIDCEWKPNYIKGSKQNKVSIMQIGSDTKIFILDLIKLYNDASEILDNCLSHILQ
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                                                                                                                                                                                                                                                                                                                                       582 AA;
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                                                                                                                                                                                                                                                                      Conservative
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556
                                                                                                                                                                                                                                                                                                                                       66467 MW;
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                                                                                                                                                                                                                                                                                      12.0%;
28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                         3_5_exonuclease
                                                                                                                                                                  GIGIDGDSVKLFHDYGVSIKDVE-----DLSDLANQKI
                                                                                                                                                                                                                                                                        36;
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Last sequ
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                                                                                                                                                                                                                                                                                      Score 179.5;
Pred. No. 6.2
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                                                                                                                                                                                                                                                                                                                                       34D752473F786680 CRC64;
                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence update)
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5.2e-08;
hes 66;
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edons; core eudicots; Rosio
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O93VS2;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence upding the control of the control 
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SEQUENCE FROM N.A.
Schulte U., Aign V., H.
Nyakatura G., Mewes H.
Submitted (FEB-2001) t
                         SEQUENCE U., Are Schulte U., Are
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                                                                                                                                                                                        Neurospora crassa.
Eukaryota; Fungi; Ascomyco:
Sordariales; Sordariaceae;
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01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
RELATED TO WERNER SYNDROME H
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Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                           NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                         93G11.60
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AP002883; BAB6/861.1; -.
AP003578; BAB60932.1; -.
NCE 494 AA; 51497 MW; 8F83F79405C2BDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69;
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ariaceae; Neurospora
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   H.W., Ma
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                                                                Hoheisel J., Brandt P.,
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                                      Mannhaupt
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Last annotation update)
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                                                                    В.,
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                                                                    Holland
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O22964; O1-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                     Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases EMBL; AC002341; AAB67629.1; -. SEQUENCE 123 AA; 13717 MW; 6481E012E6D4F3BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. COLUMBIA;
MEDLINE=20083487; PubMed=10617197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL513443; CAC28658.1; -.
InterPro; IPR002562; 3_5_exonuclease.
SMART; SM00474; 35EXOC; 1.
SEQUENCE 699 AA; 77383 MW; 42FE96D430EAB1CA CRC64;
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SEQUENCE FROM N.A.
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                                                                                                              Conservative
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Pred. No. 6.9e
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Search completed: October Job time : 31 secs

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SMART; SM00474; 35EXOC; 1. 
SEQUENCE 199 AA; 22339 MW; 6B400F2FED020899 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     "Structural analysis of Arabidopsis thaliana chromosome 5. Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AP000372; BAA96192.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Tabata S.
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ASNAYFAFGIGNILLDV
                                                                                                                                    LIVQLPDEDEGEGEDDNLPLPLFNFLNLPEFTFVGIGINKTMMRLESEFGLTCKNVVE
                                                                                                                                                                                                   TVTEKERDINRLVKTFLSNKNNRKKI--IGLDTE---RVQKGRKLNKTVLLQLC-DGDNC
                             ATDAYASWHLYKVLKDL
                                                                                                LSDLANQKIGGDKKWGLASLT-----ETLYCKELLKPNRIRLGNWEFYPLSKQQLQYA
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Viridiplantae: Streptophyta;
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195
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Post-processing: Minimum Match 0%
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   GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen
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PROA_VIBCH
Y063_CAEEL
MTC1_BACST
CA3_CCHICK
PSTS_ECOLI
PLSB_CUCSA
PMR2_APLCA
DEOC_MYCPI
E75B_DROME
E75B_DROME
C215_HUMAN
                                                                                                  UGDH_SOYBN
GYRA_CLOAB
YASB_SCHPO
6PGD_HUMAN
PHYB_SOLTU
RPE_CHLPN
6PGD_SCHPO
CH60_THEBR
GYRB_THEMA
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VL2_HPV03
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Result

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[8]
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EMBL;
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                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                   -I- FUNCTION: ESSENTIAL FOR THE FORMATION OF DNA REPLICATION FOCA CENTERS; STABLY ASSOCIATES WITH FOCI ELEMENTS GENERATING BIND SITES FOR RP-A. EXHIBITS A MAGNESIUM-DEPENDENT ATP-DEPENDENT HELICASE ACTIVITY. MAY BE INVOLVED IN THE CONTROL OF GENOMIC STABILLTY (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
-I- DISEASE: DEFECTS IN WRN ARE THE CAUSE OF WERNER SYNDROME (WS) RARE AUTOSOMAL RECESSIVE PROCEROID SYNDROME CHARACTERIZED BY PREMATURE ONSET OF MULTIPLE AGE-RELATED DISORDERS, INCLUDING ATHEROSCLEROSIS, CANCER, NON-INSULIN-DEPENDENT DIABETES MELLI (NIDDM), COULAR CATARACTS AND OSTEOPOROSIS. THE MAJOR CAUSE O DEATH (AT A MEDIAN AGE OF 47) IS MYCCARDIAL INFARCTION (MI).

-I- SIMILARITY: BELONGS TO THE HELICASE FAMILY. RECQ SUBFAMILY.
-I- SIMILARITY: CONTAINS 1 HRDC DOMAIN.
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Meisslitzer C., Ruppitsch W., Weirich-Schwaiger H., Weirich
Jabkowsky J., Klein G., Schweiger M., Hirsch-Kauffmann M.;
"Werner syndrome: characterization of mutations in the WRN 9
                                                                                                        InterPro;
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                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                        3 SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Electropean Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                         DATABASE: NAME=WRN; NOTE=WRN mutation db (Warner disease); WWW-"http://www.pathology.washington.edu/werner/ws_wrn.html"
                                     PF00271;
                                                               rPro; IPR001650; I
; PF01612; 3_5_exc
: PF00270; DEAD; 1
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277700; -.
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AF181897;
                                                                                                                                                                         AF181897; AAF06162.1; AF181896; AAF06162.1;
 SM00474;
SM00487;
SM00490;
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IPR002121;
                                                                                                                                IPR002562;
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HRDC; 1.
; 35EXOc; 1.
7; DEXDc; 1.
); HELICC; 1.
                                                                 3_5_exonuclease;
DEAD; 1.
                                                helicase_C;
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AAF06162.1;
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R., Piussan C.,
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Ogihara T.;
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ROL OF GENOMIC
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                                                        Furuichi Y.;
"Cloning of a mouse homologue of the assignment to 8A4 by fluorescence in Genomics 41:298-300(1997).
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009053; 009050; 092242;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Werner syndrome helicase homolog.
                                                                                                       STRAIN-BALB/C; TISSUE-Testis, a MEDLINE-97288537; PubMed-914351 [mamura O., Ichikawa K., Yamabe
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                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
          cells
                           Marciniak R.A.,
                                    MEDLINE=98284027;
                                               SUBCELLULAR LOCATION
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                                                                                                                                                        NCBI_TaxID=10090;
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                  284027; PubMed=9618508;
R.A., Lombard D.B., Joh
localization of the We
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Pred. No. 8
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                 Johnson
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C -> R (ASSOCIATED WITH A HIGHER
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95:6887-6892(1998).
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Sciurognathi;
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Pfam; PF00270; DEAD; 1.
Pfam; PF00271; helicase_C; 1.
Pfam; PF00570; HRDC; 1.
SMART; SM00474; 35EXOC; 1.
SMART; SM00474; JEXDC; 1.
SMART; SM00490; HELICC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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EMBL; AF091215; AAC78077.1;
MGD; MGI:109635; Wrn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
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-!- SIMILARITY: CONTAINS 1 HRDC DOMAIN.
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VKLESFVELTDVANEKLKCAETWSLNGLVKHVLGKQLLKDKSIRCSNWSNFPLTEDQKLY
                             VSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQY
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Best Local :
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01-FEB-1994 (Rel. 28, Careated)
01-FEB-1994 (Rel. 28, Last seque
01-MAR-2002 (Rel. 41, Last annot
Hypothetical 105.6 kDa protein 2
ZK1098.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Rooper A., Saunders D., Shownkeen is Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YO68_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                 Pfam; PF01612; 3_5_exonuclease; SMART; SM00474; 35EXOC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "2.2 Mb of contiguous nucleotide sequence from chromosome elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 910 AA; 1
                                                                                                                                                                                                                                                                                                                                                                   WormPep; ZK1098.8; CE00370. InterPro; IPR002562; 3_5_exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z22176; CAA80137.1; -. PIR; S40930; S40930.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wohldman P.
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FHSGIPQSLQHLIEDSTLVKVGIGIDGD------
                                  SLSDEPAPVYVGFDSEWKPSNLTAVHDSKTAIIQLFFKNCVWLVDCVELEKANMAD----
                                                                   TKRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQI---
                                                                                                                             SSTSYKRFPLSRCRARNFPAMRFGGRILY------
                                                                                                 SKLREAKELLVRRKTLQVP----LNGEQLFVFENERRTQIHMVKTESEMN----YLCSEIK
                                                                                                                                                                 TEKQ----IDAICFAIYLGIASSSS
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Last annotation
Da protein ZK1098
                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                   Score 136.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                   DB 1;
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                                                                 -----CVD---SNYCDVMHI 166
   SVKLFHDYGVSIKDVEDLSD
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RESULT 4
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                                                                                                       Matches
                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Aromatase cytochrome P450 in rat ovarian granulosa cells before and after luteinization: adenosine 3',5'-monophosphate-dependent and independent regulation. Cloning and sequencing of rat aromatase cDNA and 5' genomic DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Cytochrome P450 19 (Aromatase) (EC 1.14.14.1)
synthetase) (P-450AROM).
                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                           SEQUENCE
                                                                                                                                                                         BINDING
                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                EMBL; M33986; AAA41044.1; PIR; A36121; A36121
                                                                                                                                                                                                                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Endocrinol. 4:3-12(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90220647; PubMed=2157976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYP19 OR AROM.
                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                    InterPro; IPR001128;
 158
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                                                                            93 RFGGRILYSKTATEVDKRAMOLIKVLDTKRDESGIAFVGLDIEW---RPSFRKGVL-PGK 148
                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: RH + reduced flavoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: CATALYZES
                                                                                                                                                                                                                                                                                                                                                                                                                                       oxidized flavoprotein
                           VATVQICVD---
IRMVEVCVESIKQHLDRLGDVTDNSGYVDVVTL-----
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                                                                                                                                                                                                                                      PF00067; p450;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANDROGENS
                                                                                                                     Similarity
                                                                                                                                                                                                                          PR00385;
                                                                                                                                                                                           PS00086; CYTOCHROME_P450; 1.
+r=n=nort: Oxidoreductase; Monooxygenase; Membrane;
                                                                                                                                                           437
508 AA;
                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: Membrane-bound.
BELONGS TO THE CYTOCHROME P450 FAMILY.
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58411 MW;
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Rodentia;
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                         -SNYCDVMHIFHSGIPQSLQHLIED-STLVKVGIGID
                                                                                                     Pred. No. 1.4;
5; Mismatches
                                                                                                                                Score 95;
                                                                                                                                                           HEME.
; COADFB0FD80AB352 CRC64;
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF AROMATIC
                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                              Usage
 -MRHIMLDTSNTLFLGIPLD
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Murinae; Rattus
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RESULT
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               R InterPro; IPR000157; Flavi_N.S.1.
R InterPro; IPR000157; Flavi_NS1.
R InterPro; IPR000157; Flavi_NS2B.
R InterPro; IPR000187; Flavi_NS2B.
R InterPro; IPR0001122; Flavi_Capsid.
R InterPro; IPR000336; Flavi_Gapsid.
R InterPro; IPR000336; Flavi_Dropep.
R InterPro; IPR0002535; Flavi_Dropep.
R Pfam; PF01003; Flavi_Gapsid; 1.
R Pfam; PF01004; Flavi_NS2B; 1.
R Pfam; PF01005; Flavi_NS2B; 1.
R Pfam; PF0105; Flavi_NS2B; 1.
R Pfam; PF01056; Flavi_NS2B; 1.
R Pfam; PF01570; Flavi_NS2B; 1.
R Pfam; PF01570; Flavi_NS2B; 1.
R Pfam; PF01570; Flavi_Dropep; 1.
R Pfonom; PD001496; Flavi_SC; 1.
Variable Protein; Glycoprotein; Core protein; Coat protein; Pp001570; Hydrolase; Helicase; ATP-binding; Transivations of the protein; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trent D.W., Kinney R.M., Johnson B.J.B., Deubel V., Rice C.M., Hahn C.; Partial nucleotide sequence of St. Louis structural proteins, NS1, NS2A, and NS2B. Virology 156:293-304(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last annotation update) Genome polyprotein (Contains: Capsid protein Genome polyprotein M); Major envelope protein M); Major envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M16614; AAA47786.1; PIR; A27531; GNWVS5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <del>-</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE FUNCTION NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION. CATALYTIC ACTIVITY: HYDROLYSIS OF FOUR PEPTIDE BONDS IN THE PRECURSOR POLYPROTEIN, COMMONLY WITH ASP OR GLU IN THE P6 POSITION, CYS OR THR IN P1 AND SER OR ALA IN P1. SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED
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Q88783; Q88784; Q88785; Q88786; Q88787;
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Cripe L.D., Moore K.D., Kane W.H.;
"Structure of the gene for human coagulation
Blochemistry 31:3777-3785(1992).
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NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
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SEQUENCE FROM N.A.

MEDLINE=87260886; PubMed=3110773;

Jenny R.J., Pittman D.D., Toole J.J., Kriz R.W., A
Hewick R.M., Kaufman R.J., Mann K.G.;

"Complete cDNA and derived amino acid sequence of
"Complete cDNA and Sci. U.S.A. 84:4846-4850(1987).
                                                                                                                                               Bertina R.J., de Ronde H., van der Velden P.A., Reitsma P.I "Mutation in blood coagulation factor V associated with r activated protein C.", Nature 369:64-67(1994).

-I FUNCTION: COAGULATION FACTOR V IS A COFACTOR THAT PARTURE THE FACTOR XA TO ACTIVATE PROTHROMBIN TO THROMBIN.

-I SUBUNIT: Factor Va is composed of a heavy chain and a chain, noncovalently bound. The interaction between the substitute of the composed of the comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-20052169; PubMed-10586886; MEDINE-20052169; PubMed-10586886; Macedo-Ribeiro S., Bode W., Huber R., Quinn-Allen Ortel T.L., Bourenkov G.P., Bartunik H.D., Stubbs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc.
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Kane W.H., Ichinose A., Hagen F.S.,
"Cloning of cDNAs coding for the hea
region of human factor V, a blood co
of internal repeats.";
Biochemistry 26:6508-6514(1987).
                                                                                                                                                                                                                                                                                                                                                                                                       "Crystal structures of coagulation factor V."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pittman D.D.,
Kaufman R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93203619; PubMed-8454869; chen N.L.L., Fan S.-T., Pyati J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Fuentes-Prior P.;
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MEDLINE~86313665; Publ
                                                                                                                                                                                                                                                                                                                             MEDLINE=94217810; PubMed=8164741;
                                                                                                                                                                                                                                                                                                                                                 VARIANT APCR GLN-534
                                                                                                                                                                                                                                                                                                                                                                                       Nature 402:434-439(1999).
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                cofactor, factor Va (formation of a heavy chain atterminus and a light chain at the C-terminus).
PTM: SULFATION IS REQUIRED FOR EFFICIENT THROMBIN
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76:946-952(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ng of a cDNA coding for human homologous to factor VIII and Natl. Acad. Sci. U.S.A. 83:680
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PubMed=3092220;
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  PROCOAGULANT
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SMART; SM0231; FA58C; 2.

RPROSITE; PS00079; MULTICOPPER_OXIDASE1; 2.

RPROSITE; PS01285; FA58C_1; 2.

R PROSITE; PS01286; FA58C_2; 2.

R Blood coagulation; Glycoprotein; Sulfation; Glycoprotein; Sulfation; Glycoprotein; Sulfation; Tlycoprotein; 
                                                                                                                                                                                                                                                  InterPro;
Pfam; PFO(
Pfam; PFO(
                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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1; A25897; A25897.

1; A26828; A26028.

1; ICZS; 26-NOV-99.

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SIMILARITY: CONTAINS 3 F5/8 TYPE A DOMAINS: EACH IS COMPOSED OF 2 PLASTOCYANIN-LIKE REPEATS.

SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.

SIMILARITY: STRONG, TO COAGGLATION FACTOR VIII.
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1CZT; 26
1CZV; 26
134400;
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227310;
227400;
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L32775;
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M16967;
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PF00754; F5_F8_type_C; 2.
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L32755; AAB59401.1;
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0394; Cu-oxidase; 3.
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Query Match
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EMBL; X75449; X75449; CAA9300
EMBL; Z74823; CAA9309
PIR; S11190; RGBYIZ
SGD; S0005441; IRA2.
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SMART; SM00323; RASGAP; 1.
PROSITE; PS00509; RAS_GTPASE_ACTIV_1; 1.
PROSITE; PS50018; RAS_GTPASE_ACTIV_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and RAS2 gene products.";
Curr. Genet. 21:325-329(1992).
-!- FUNCTION: INHIBITORY REGULATOR
STIMULATES THE GTPASE ACTIVITY
-!- SIMILARITY: CONTAINS 1 RAS-GAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bussereau F., Dupont C.H., Boy-Marcotte E., Mallet L., Jacquet "The CCS1 gene from Saccharomyces cerevisiae which is involved mitochondrial functions is identified as IRA2 an attenuator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tzermia M., Katsoulou C., Alexandraki D.;
"Sequence analysis of a 33.2 kb segment from the left arm of chromosome XV reveals eight known genes and ten new open reat frames including homologues of ABC transporters, inositol phosphatases and human expressed sequence tags.";
Yeast 13:583-589(1997).
                                                                                                             CONFLICT
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"Sequence of a 10.27 kb segment on the left arm of chromosome Saccharomyces cerevisiae includes part of the IRA2 gene and a putative new gene.";
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MEDLINE=90318397; PubMed=2164637;
Tanaka K., Nakafuku M., Tamano1 F., Kaziro Y., Matsumoto K., Tanaka K., Nakafuku M., Tamano1 F., Kaziro Y., Matsumoto K., Tanaka K., a second gene of Saccharomyces cerevisiae that encodes
                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION OF CCS1 AS IRA2.
MEDLINE=92405229; PubMed=1326414;
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MEDLINE=95208358; PubMed=7900427;
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protein.";
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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10:1383-1387(1994).
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IPR001936; RasGAP.
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                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                          McDougall R., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
-i- CATALYTIC ACTIVITY: 3-ISOPROPYLMALATE = 2-ISOPROPYLMALEATE
H(2)0 (ALSO CATALYSES 2-ISOPROPYLMALEATE + H(2)0 = 3-HYDRO)
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the European Bioinformatics Institute
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                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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            ; Iron-sulfur; 4Fe-4S.
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P36744;
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                                                                                                                                                                                                EMBL; X74462; CAA52473.1; PIR; S36553; S36553.
                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entities requires a license agreement (See http://www.isb
                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                  Delius H., Hofmann B.;
"Primer-directed sequencing of human papillomavirus types.";
Curr. Top. Microbiol. Immunol. 186:13-31(1994).
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=94265501; PubMed=8205838;
                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus type 3 Viruses; dsDNA viruses, no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSNYCDVMHIF----HSGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SR-----CRARNFPAMRFGGRILYSKTATEVDKRAM-----QLIKVLDTKRDESGI--AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --SDLANQKIGGDKKWGLASL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGLDIEWRP---SFRKGVLPGKVATVQIC-----V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEAGFDWREAGCSMCLGMNPDQLKPYERCASTSNRNFEGRQGAKGRTHLVSPAMAAAAAI
                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 29, Created)
(Rel. 29, Last seq
(Rel. 34, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34, Last sequence up
14, Last annotation on L2.
                                                                                               6.1%;
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                                                                                  34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA stage; Papillomaviridae;
                                                                                Score 91.5; DB Pred. No. 2.6; 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 92; [
Pred. No. 4.
                                                                                                                                         DD8298FE517A04DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                      <u>-</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473
                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TETLVCKELLKP-NRIRLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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                                                                                                            DB 1;
                                                                                   95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 758
                                                                                                             Length 473;
                                                                                   Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --DIGLSVDDATDAV
                                                                                                                                                                                                                                                                                             restrictions
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                                                                                                                                                                                                                                                                   for commercial
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                                                                                Gaps
                            195
                                                      60
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Matches Query Match Best Local

38; Conser

Conservative

23;

Mismatches

ω ..

70;

Gaps

8

6.18;

Score 91; Pred. No.

DB 1;

Length 503;

BINDING SEQUENCE

503

A K

HEME (BY SIMILARITY).
; 737400389D1AEFF1 CRC64;

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RESULT 10
CPV1_MOUSE
ALD DEPTH OF THE PROPERTY OF T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P28649;
01-DEC-1992
01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Ovary;
TISSUE-Ovary;
MEDLINE-91378248; PubMed-1897929;
Merashima M., Toda K., Kawamoto T., Kuribayashi I.,
                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation of a full-length cDNA encoding mouse aromatase P450."; Arch. Biochem. Biophys. 285:231-237(1991).
-!- FUNCTION: CATALYZES THE FORMATION OF AROMATIC C18 ESTROGENS F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Cytochrome P450 19 (Aromatase) (EC 1.14.14.1)
synthetase) (P-450AROM).
                                                                                                                                                MGD: MGI:88587; Cyp19.
InterPro; IPRO01128; Cyt_P450
Pfam; PF00067; P450; 1.
                                                                                                                                                                                                                                                                                                                or send an email t
                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C19 ANDROGENS.
-!- CATALYTIC ACTIVITY: RH + reduced flavoprotein oxidized flavoprotein + H(2)0.
-!- SUBCELLULAR LOCATION: Membrane-bound.
                                                                            Electron transport; Oxidoreductase; Monooxygenase; Membrane;
                                                                                                    PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450;
                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYP19 OR AROM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CPV1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDADIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----HSGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIG
                                                                                                                                                                                                                                                               D00659;
                                                                                                                                                                                                                                                                                                                an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366
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$13912. ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                            license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMRTRSGKGL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                         http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muridae;
                                                                                                                                                                                                                                                                                                                                                               Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GARVHYYQDLSPIGP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CYPXIX) (Estrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -ASASAYDS--LYDVYADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C18 ESTROGENS FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0(2)
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ogawa
                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaboration - MBL outstation
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                                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                outstation
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RESULT 11
DOD_HAEIN
ID OLHAEIN
ID OLHAEIN
ID OLHAEN
AC P43741
DT 01-NOV
DT 0
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SEQUENCE FROM N.A.

C STRAIN=RD / KW20 / ATCC 51907;

C STRAIN=RD / KW20 / ATCC 51907;

X MEDLINE=95350630; PubMed=7542800;

XA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

RA Kerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M.,

RA MCKenney K., Sutton G., Fitchugh W., Fields C.A., Gocayne J.D.,

RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

RA Weidman J.F., Phillips C.A., Spridgs T., Hedblom E., Cotton M.D.,

RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Chahm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dр
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                                                                                                                                                                                                                                                                                                              EMBL; U32767;
HSSP; P00582;
TIGR; HI0856;
                                                pfam; PF01612; 3_5_exonuclease; pfam; PF01367; 5_3_exonuclease; pfam; PF02739; 5_3_exonuc_N; 1. Pfam; PF00476; DNA_pol_A; 1.
                                                                                                                                                   InterPro: IPR002562; 3_5_exonuclease. InterPro: IPR002421; 5_3_exonuclease. InterPro: IPR002298; DNA_polI. InterPro: IPR001098; DNA_pol_A. InterPro: IPR000513; Exo_N_I. InterPro: IPR000514; HHH_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 269:496-512(1995).
-!- FUNCTION: IN ADDITION TO EXHIBITS 3' TO 5' AND 5'
                                                                                                                                                                                                                                                                                                                                                                                                              or send
                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria;
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SMART; SM00279; HhH2; 1.
SMART; SM00279; HhH2; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
PROSITE; PS00447; DNA_DOLYMERASE_A; 1.
Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase; Exonuclease; DNA-binding; Complete proteome.
Hydrolase; Exonuclease; DNA-binding; Complete proteome.
Hydrolase; Aqn AA: 103740 MW; 226654BB7CFF730B CRC64;
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Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft
Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
Langham S.-A., McCullagh B., Bilham L., Robben J.,
                                                                  MEDLINE=20083488; PubMed=10617198; Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckae Mayer K.F.X., Schueller C., Wambutt R., Entian K.-D., Terryy Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryy Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Weichselgartner M., de Simone V., Obermaier B., Mache R., Weichselgartner M., Puigdomenech P., Watson M., Schmidth, Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidth, Beibert M., Delseny M., Puigdomenech P., Watson M., Schmidth, Beibert M., Delseny M., Puigdomenech P., Watson M., Schmidth, Beibert M., Delseny M., Puigdomenech P., Watson M., Schmidth, Beibert M., Delseny M., Puigdomenech P., Watson M., Schmidth, Beibert M., Delseny M., Puigdomenech P., Watson M., Schmidth, Beibert M., Delseny M., Puigdomenech P., Watson M., Schmidth, Beibert M., Delseny M., Puigdomenech P., Watson M., Schmidth, Beibert M., Beibert M.
                                                                                                                                                                                                                                                                                                     STRAIN-CV. COLUMBIA;
MEDLINE-99444907; PubMed-10517319;
MEDLINE-99444907; PubMed-10517319;
Doutriau
John Helzile F., Philippe H., Doutriau
"Four mismatch repair paralogues coexist
AtmSH2, AtmSH3, AtmSH6-1 and AtmSH6-2.";
Mol. Gen. Genet. 262:239-249(1999).
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Till S., Granat S., Parnell L., Kaplan N., Hoffman J., I
Johnson A.F., Dedhia N., Martienssen R., McCombie W.R.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta: Magnoliophyta; eudicotyle
eurosids II; Brassicales; Brassicaceae;
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RA Bernelser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Pettett A., Rajandream M.A., Lyne M., Lennard N., McLay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller Auer S.,
RA Glabel C., Fuchs M., Maarse A.C., Schaefer M., Mueller Auer S.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbbl M., Bargues M., Terol J., Torres A.,
RA Pergez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Pergell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Schnahl S., Haller N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Schnahl S., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Alley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Alley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Marper J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Pepin K., Hillier L.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Pepin K., Hillier L.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.;
RL Lauteria M., Martienssen R., McCombie W.R.;
RL Lauteria M., Martienssen R., McCombie W.R.;
                                                                                                                                                                                                                                                                                 EMBL; AF001308; AAC78699.1; -.
EMBL; AL161493; CABB0700.1; -.
InterPro: IPR000432; Muts_C.
InterPro: IPR002863; Muts_N.
InterPro: IPR002999; Tudor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions are nowed. Usage by ancondition and this statement is not removed.
                                                                                                                                                               SMART; SM00534; MUTSac; SMART; SM00533; MUTSd; 1 SMART; SM00333; TUDOR; 1
                                                                                                                                                                                                                       Pfam; PF00488; MutS_C; 1.
Pfam; PF01624; MutS_N; 1.
ProDom; PD001263; MutS_C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THALLAGE ().
NATURE 402:769-777(1999).
--- FINCTION: INVOLVED IN POST-REPLICATIVE DNA-MISMATCH REPAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braum Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W. Mooljman P., Klein Lankhorst R., Rose M., Hauf J., Koetter
                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                        EMBL:
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL:
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                                                                                                                          DNA repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - !- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                  AF001535; AAB57798.1; -. AJ245967; CAB53337.1; -.
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                                                                                                                                      PS00486; DNA_MISMATCH_REPAIR_2; 1.
                                     ; ATP-binding; I
1083 1090
316 318
383 383
852 852
                                                                                                                                                               TUDOR; 1.
  AA;
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  146797
                                                                                                                        DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF MSH2 AND MSH6
    ₹.
                                 ATP (PÓTENTIAL).

ADR -> GKPKSLLL (IN REF. 1).

Q -> QVRRAHGNL (IN REF. 1).

P -> PGIINLLHIHILILANCTASHIISLP
                      REF
787A340272CF979C CRC64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 moved. Usage by and for (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GTBP)
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den Daele
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Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Awan K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Caddieu E., Center A., Chandra I.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
And Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
And Cherry J.M., Cawley S., Davies R.,
And Cherry J.M., Cawley S., Davies R.,
And Cherry J.M., Cawley S., Davies R.,
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9VGI8; Q9Y062; 01-MAR-2002 (Rel. 41, Created) 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) 01-MAR-2002 (Rel. 41, Last annotation update) Bloom's syndrome protein homolog (EC 3.6.1.-) sensitive protein 309) (RecQ helicase homolog) mus309 or blm or CG6920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Berkeley;
MEDLING-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kusano K., Berres M.E., Engels W.R.; "Evolution of the RECQ family of helicases: a Drosophila homolog, Dmblm, is similar to the human Bloom syndrome gene."; Genetics 151:1027-1039(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99160561; PubMed=10049920;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pterygota; Neoptera;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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era; Muscomorpha;
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshreti A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Pittnan G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradding A.C., Stapleton M., Skupski M.P., Smith T.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Poodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).

CC '- FUNCTION: Participates in DNA replication and may participate in
CC repair Exhibits a magnesium dependent ATP-dependent DNA-helicase
CC activity that unwinds single- and double-stranded DNA in a 3'-5'
CC direction (By similarity).

CC '- SUMSIEARIUAR LOCATION: Nuclear (By similarity).

CC '- SIMILARITY: BELONGS TO THE HELICASE FAMILY. RECQ SUBFAMILY.
                                                                                              CONFLICT
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Pfam; PF00570; HRDC; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
SMART; SM00341; HRDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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InterPro; IPR001410; DEAD.
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DOMAIN 89
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InterPro; IPR002121;
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"Expression of zebrafish nk2.2 is influenced by sonic

"Expression of zebrafish nk2.2 is influenced by sonic

hedgehog/vertebrate hedgehog-1 and demarcates a zone of neuronal
hedgehog/vertebrate hedgehog-1 and demarcates.";

differentiation in the embryonic forebrain.";

Development 121:1755-1768(1995).

10-verlopment 121:1755
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Homeobox protein NKX-2.2.
NKX2-2 OR NKX2.2 OR NK2.2.
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                                                                                                                                                                                 modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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Eukaryota; Metazoa; Chordata; Craniata; Vert
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                   InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                             HSSP; P22808; 1NK3.
ZFIN; ZDB-GENE-980526-403; nkx2.2.
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                                                                                                              EMBL;
                                                                                                                                                          or send
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                                                                                                                                                                                                                                                                                                                                            ALONG A BOUNDARY ZONE DEMARCATING THE LOCATION AT WHICH TWO EARLIEST NUCLEI IN THE BRAIN DIFFERENTIATE. SIMILARITY: BELONGS TO THE NK-2 FAMILY OF HOMEOBOX PROTEINS
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RESULT 15
PROA_V
AC Q9KPT9
DT 16-QCT
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DT 16-QCT
DT 6-QCT
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               modified entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Bodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Cill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P. McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McDonald L., Utterback T.,
Salzberg S.L., Smith H.O.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
Gamma-glutamyl phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-5-
semialdehyde dehydrogenase) (Glutamyl-gamma-semialdehyde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homeobox; DNA-binding; Developmental protein; Nuclear protein DNA_BIND 125 184 HOMEOBOX. SEQUENCE 269 AA; 30306 MW; CF006285CDD33D63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-EL TOR N16961 / SEROTYPE 01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio cholerae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dehydrogenase) (GSA
PROA OR VC2273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
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                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lifted and this statement is not removed. Usage by and for commercial itself and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: L-glutamate 5-semialdehyde + phosphate NADP(+) = L-gamma-glutamyl 5-phosphate + NADPH. PATHWAY: PROLINE BIOSYNTHESIS PATHWAY; SECOND STEP.
                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE GAMMA-GLUTAMYL PHOSPHATE REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: CATALYZES THE NADPH DEPENDENT REDUCTION OF L-GAMMA-GLUTAMYL 5-PHOSPHATE INTO L-GLUTAMATE 5-SEMIALDEHYDE AND PHOSPHATE. THE PRODUCT SPONTANEOUSLY UNDERGOES CYCLIZATION TO
                                                                                                                                                                                                                                                                                                                                                                                                                1-PYRROLINE-5-CARBOXYLATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNGSDSGKKRKR
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itions as it is not removed. Usage by is not removed that is not removed.
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Best Local :
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SEQUENCE 416 AA; 44504 MW; 7ACA58E537235563
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PROSITE; PS01223; PROA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002086;
InterPro; IPR000965;
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WLSYTLGVKVVQDVQEAI
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                                                                                                         -GFGISHIFVDESADLDKSVAVIENAKV--QRP
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Search completed: October 31, 2002, 13:42:17 Job time : 20 secs

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Score
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Copyright (c) 1993 - 2002 Compug
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protein kinase-114
DNA-directed DNA p
mismatch repair en
nk2.2 protein - ze
                                                                                                                           hypothetical prote aromatase (EC 1.14
                                                                                               genome polyprotein
coagulation factor
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hypothetical prote agmatinase [import
                                                                      hypothetical prote
3-isopropylmalate
                                                                                      coagulation factor probable GTPase-ac
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Werner syndrome pr
probable 3'-5' exo
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DNA helicase 1 - A
                                                               L2 protein
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
86.5	86.5	86.5	86.5	86.5	87	87	87	87	87.5	87.5	87.5	87.5	88	88	88
5. 8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.9	5.9	5.9	5.9	5.9	5.9	5.9
593	496	470	360	346	3137	579	392	178	589	547	422	334	784	709	417
N	δ	N	2	Н	<u> </u>	N	N	2	N	N	Ν	N	N	N	2
В89844	S61966	T10193	T00882	BYECPR	A37797	I40371	T44362	E72450	E88492	T40342	E96753	T03556	C88558	S40926	E82095
hypothetical prote	hypothetical prote	glycerol-3-phospha	hypothetical prote	phosphate-repressi	collagen alpha 3(V	methyltransferase	acetyl-CoA C-acety	hypothetical prote	protein T07E3.1 [i	signal recognition	hypothetical prote	probable D-ribose-	protein ZK1098.3 [hypothetical prote	gamma-glutamyl pho

ALIGNMENTS

3

DNA helicase 1 - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 C;Accession: T14895 R;Yan, H.; Chen, C.Y.; Kobayashi, R.; Newport, J. RESULT T14895 hypothetical protein F18A5.260 - Arabidopsis thaliana
()Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C;Accession: T05256
R;Bevan, M.; Weber, N.; Grueninger, D.; Schmidheini, T.; Bancroft, I.; Mewes,
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15405
A;Accession: T05256
A;Molecule type: DNA
A;Residues: I-313 <BEV>
A;Experimental source: cultivar Columbia; BAC clone F18A5.
C;Genetics: Qy 밁 Qy 밁 QY 멍 Qy 밁 δõ A; Map position: 4 A; Introns: 86/1; 3 A; Note: F18A5.260 Best Loca Matches Query Match 241 181 181 121 121 H.; Chen, C.Y.; Kobayashi, R.; Newport, J. Genet. 19, 375-378, 1998 N 61 61 Local 1 MSSSNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSAAPTVQATTSVHGHEEDPNQIPN DSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKEL KRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLIE NIRRQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDT 120 KRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLIE NIRRQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDT MSSSNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSSAAPTVQATTSVHGHEEDPNQIPN 281; Similarity Conservative 143/1; 186/3; 239/3 96.5%; Pred. No. 6e-117; 1; Mismatches Score 1439.5; DB #text_change 4; 2; Indels Length 313; 20-Sep-1999 9; 286 Gaps 180 60 60 240 180 120 240 ۳ H.W.;

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R:Imamura, O.; Ichikawa, K.; Yamabe, Y.; Goto, M.; Sugawara, M.; Furuichi, Y. Genomics 41, 298-300, 1997
A:Title: Cloning of a mouse homologue of the human Werner syndrome gene and assignment A:Reference number: 220785; MUID:97288537
A:Accession: T30247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: Wrn typeI protein c;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000 C;Accession: T30247
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A;Accession: T14895
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1436 <YAN>
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A; Residues: 1-1401 < IMA>
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Best Local
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207
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                                                                        VSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQY
                                                                                                                    NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIF-
                           AATDAYASWHLYKVLKDLPDAV
                                                          VKLESFYELTDVANEKLKCAETWSLNGLVKHVLGKQLLKDKSIRCSNWSNFPLTEDQKLY
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                                                                                                                                                                                    NLPFLEFPGSIVYSYEASD----CSFLSEDISMRLSDGDV--VGFDMEWPPIYK----PG
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35.0%;
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Pred. No. 8.0
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1.6e-21;
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GCRVVGIDCEWKPNYIKGSKQNKVSIMQIGSDTKIFILDLIKLYNDASEILDNCLSHILQ

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probable 3'-5' (C;Specier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable 3'-5' exonuclease [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C:Accession: H96604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Paeper, B.W.; Gayle, M.; Brady, W.; Swartz, A.; Gillett, L.A.; Alisch, R.S.; submitted to the EMBL Data Library, September 1998 A;Description: Genomic structure of the human Werner's gene and cloning of its A;Reference number: 218794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: Wrn protein
C;Species: Mus musculus (house mouse)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
δõ
                                                                                                                            A;Map
                                                                                                                                               C; Genetics:
A; Gene: F14G9.8
                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-582 <STO>
                                                                                                                                                                                                                                                                   A; Reference number: A86141;
A; Accession: H96604
                                                                                                                                                                                                                                                                                                                                                                                                                                      Chin, C.W.; Chung, M.K.; Conn, L.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dev
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A; Residues: 1-1401 <PAE>
A; Cross-references: EMBL
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R; Paeper, B.W.; Gay
                                                                                                                                                                                        A;Cross-references:
                                                                                                                                                                                                                                                    A;Status: preliminary
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Best Local
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    GIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSN--YCDVMHIFHSG---IPQSLQHLIE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATDAYASWHLYKVLKDLPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLPFLEFPGSIVYSYEASD----CSFLSEDISMRLSDGDV--VGFDMEWPPIYK----PG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKLESFVELTDVANEKLKCAETWSLNGLVKHVLGKQLLKDKSIRCSNWSNFPLTEDQKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQY 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATDAYAGLIIYQKLGNLGD
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                                             Conservative
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                                                              12.0%;
28.2%;
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                                             36;
                                                              Score 179.5;
Pred. No. 1.
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3; Mismatches
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                                             Mismatches
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No. 5
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Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein ZK1098.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #te
    Вb
                                                                                                                  Qy
                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-910 <THO>
A;Cross-references: EMBL:Z22176; NID:g297978; PID:g297986
                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data A; Reference number: $40923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487
A;Accession: E84752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
E84752
E94752
hypothetical protein At2g34110 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: E84752
                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: $40930
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A:Map position: 2
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A; Residues: 1-123 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references:
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                                                                                                                                                                                                           Query Match
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369 SKLREAKELLVRRKTLQVP---LNGEQLFVFENERRTQIHMVKTESEMN----YLCSEIK 421
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                                             72
                                                                                                                       12 TEEELLAIDAIEASYNFSRSSSSSSSSAAPTVQATTSVHGHEEDPNQIPNNIRRQLPRSIT 71
                                                                                                                                                                                        Local
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                                         SSTSYKREPLSRCRARNEPAMREGGRILY----
                                                                                  TEKQ --- IDAICFAIYLGIASSS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKSTLKLVSLTEDYPDHKLSSGYNFQCDIKQLALSYG-DLKCFERYDMLLDIQNVFNEPF 495
                                                                                                                                                                                                                                                  64/1;
                                                                                                                                                                    Similarity
77; Conser
                                                                                                                                                                                                                                                336/2; 382/2; 447/2; 681/2; 810/1; 852/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #sequence_revision 06-Jan-1995 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.6%;
                                                                                                                                                                                   9.2%; Score 136.5; DB 2; 24.8%; Pred. No. 0.0018;
                                                                                                                                                                                                                                                                                                                                                                                                                     Library, February
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Pred. No. 1.6e-06;
                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                       1992
                                         SKTATEVDKRAMQLIKVLD 119
                                                                                  ---YQLP-NVMRDFFRQPD
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hypothetical protein At2g32490 [imported] - Arabidopsis thaliana N. Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change iC; Accession: T02548; G84733 R; Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; submitted to the EMBL Data Library, July 1998 A; Description: Arabidopsis thaliana chromosome II BAC T26B15 gence A; Reference number: Z14678 A; Accession: T02548 A; Baccession: T02548 A; Status: translated from GB/EMBL/DDBJ A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
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A; Map position: 2
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A; Residues: 1-239 <STO>
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                                                                                                                                                                                                                                                                                                         RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                        LTETLYCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAY 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDETITFVGVWNSQDQGKLERFRHQLEIWRLLDIRHYLPTRLLNSSFEKI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDSTLVKVGIGIDGDSVKL---FHDYGV-SIKDVED-----LSDLANQKIGGDKKWGLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRSSHPLV-VGLDVQWTP----GGSDPPPDILQLCV-GNRCLIIQLSHCKRIPEVLRSFL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFH-SGIPQSLQHLI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRRRIQKRHIHENRYIDF-------FGERLIVTVTHTTSTIRRWIHSIRFFSR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAYASWHLYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                           K.A.; Crosby, M.L.;
                                                                                             II BAC T26B15 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                                                           Brandon, R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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T19246
C: Species: Caenorhabditis elegans
C: Species: Caenorhabditis elegans
C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tc
C: Accession: T19246
R: MCMUXTRY, A.
Submitted to the EMBL Data Library, June 1995
A: Reference number: Z19097
A: Accession: T19246
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A; Cross references: GB: AE002093; C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-217 <ROU>
A;Cross·references: EMBL:AC004681; NID:g3298532; PID:g3298537
A;Cross·references: EMBL:AC004681; NID:g3298532; PID:g3298537
A;Experimental source: cultivar Columbia
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                  A;Gene: CESP:C14A4.4
A;Map position: 2
A;Introns: 80/2; 557,
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A; Residues: 1-876 <WIL>
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A; Introns: 25/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                       Query Match
Best Local 9
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Best Local (
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                                                                                  65
                                                                                                                                                        15 ELLAIDAIEASYNFSRSSSSSSSAAP-----TVQATTSVHGHEEDPNQIPNNIRR
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                                                                                                                   QMVVLEKPQKTYNI----SSDNSQAPFSSKLTVKHHAIEKRTGIVLHDDDESG-----RR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VHIRHYLHPLL-----LSSSFETIVKVYLGHEGVTKDKELCMSNWGARSLSHDQIVQA
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LDTKRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICV-DSNY-CDVMHIF-HSGIPQS
                                                                            QLPRSITSS-----TSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGERLIVTVTHTPSVIRRWIHSIRFVSRLRLSHPLV-VGLGVQWTP---RGSDPPPDI--L
                                         DWISAETETEEEHPYIAEILHFKVPEAQLKSAECLKFTALKDTPLTMIDTKEKLEALTKT
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80/2; 557/2; 731/3; 833/1
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21.1%;
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25.4%;
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Pred. No. 0.03;
38; Mismatches
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                                                                                                                                                                                                                       Score 101;
Pred. No. 2;
                                                                                                                                                                                                  Mismatches 125;
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  174
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1

hypothetical protein CAC1132 [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: F97039 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gib R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gib

A; Title: Genome Sequence and Comparative Analysis of the A; Reference number: A96900; MUID:21359325; PMID:21359325

.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; J. Bacteriol. 183, 4823-4838, 2001

Smith, D. Markarova, K.S.; Smith, D.R.

Solvent-Producing Bacterium

Q.; Gibson,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-445 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Complete genome sequence of an aerobic hyper-thermophilic A; Reference number: A72450; MUID:99310339
A; Accession: E72674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y
DNA Res. 6, 83-101, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: E72674
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics:
186
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DRLRYLRMALEELG - - -
                                 NRIR-----LGNWEFYPLSKQQL-----QYAATDAYASWHLYKVLK
                                                                                                         VKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKI-GGDKKWGLASLTETLVCKELLKP
                                                                                                                                                DVDRLVRLVAEWARA-----NPASAKVFLDS-----LSAELERL-----
                                                                                                                                                                                                                        VSRA-YFYQMRRGLR-----PISDSILERLLELATDDDLAGIPFFAPYVDYQRVKGY 115
                                                                                                                                                                                                                                                          RCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFV------GL 132
                                                                                                                                                                                                                                                                                                 SKNSTAAPSSSHAEGESTADVLGYEGVEVLPEPKDVPQEARRQLLNLLAERGKVKPSTLG 64
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                                                                      -----GLVGKAIK-----VSERHVREFEGYLEARVRSGDMDPGTAG-----
                                                                                                                                                                                 DI-----EWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLIEDSTL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRFADVVLDKQYQLADWRARPLRNAMINYAREDTHYLLYSYDMLREQLLKQDTKDLANVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNEPFANPRILKVFHGSDSDVLWLQRDYGVHVVNLFD-TYVAMKKL-KYPKFSLAYL--T
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-YVLTKQALRGLIRRYQASQPGVADHIYKSLK
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Pred., No. 1.6;
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 230
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Ta J.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Aromatase cytochrome P450 in rat ovarian granulosa matase cDNA and 5' genomic DNA.
A; Reference number: A36121; MUID:90220647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change C;Accession: A36121; S16901; S26817 R;Hickey, G.J.; Krasnow, J.S.; Beattie, W.G.; Richards, J.S. Mol. Endocrinol. 4, 3-12, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
A36121
                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-2,'FQ',5-9,'Q',11-87,'C',89-100,'L',102-122,'VVH',126,'HAR',130-187,'L',18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:M33986; NID:g203804; PIDN:AAA41044.1; PID:g203805 R;Lephart, E.D.; Peterson, K.G.; Noble, J.F.; George, F.W.; McPhaul, M.J. Mol. Cell. Endocrinol. 70, 31-40, 1990
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Mosidues: 1-488 < KURN
A;Residues: 1-488 < KURN
A;Cross-references: GB:AE001437; PIDN:AAK79105.1; PID:g15024051; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
C;Genetics:
A;Gene: CAC1132
                                                                                                                                                                                                                                                                                                                                                             A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S16901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: The structure of cDNA clones encoding
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A; Residues: 1-508 <HIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Rattus norvegicus (Norway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N; Alternate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aromatase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number:
                                                                                                                                                                                                                                                                                     437/Binding site:
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                   Query Match
Best Local
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                                      193
                                                                        158
                                                                                                           149
                                                                                                                                              115
210 ESSIVKKIQGYFNAWQALLIKPNIFFKISWLYRKYERSVKDLKDEIEILVEKKRQKVSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 TATEVDKRAMQLI-KVLDTKRDESGIAFVGLDIEW-----RPSFRKGVLPGKVATVQ 153
                                                                                                                                                                               93
                                                                                                                                                                                                                Local Similarity 23.1 nes 42; Conservative
                                                                                                                                                                                                                                                                                                                                                               CYP19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                      GDSVK - - -
                                                                                                         VATVQICVD---
                                                                    IRMVEVCVESIKQHLDRLGDVTDNSGYVDVVTL-----MRHIMLDTSNTLFLGIPLD
                                                                                                                                        RFG----SKRGLQCIGM-----HENGIIFNNNPSLWRTVRPFFMKALTGPGL 157
                                                                                                                                                                           RFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEW---RPSFRKGVL-PGK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EC 1.14.14.-) cytochrome P450 19 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVILNVYPVTIKYDSIENEEENEMAEKKKNPKKK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --AELNYNQVMLSLRSQLKDNLGDCYWNFYIFSNGVDFLVMENYDDGSLVRIDFTVDGDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ICVDSNYCDVM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKLFHDYGVSIK----DVEDLSDLANQKIGGDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPAVVSAKATKLVAELLNIKESENEMVKKINPLEWEEKILAELKKSYRRTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     names: cytochrome P450 arom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                   iron (Cys) (axial ligand) #status
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                                                                                                                                                                                                                               6.4%; Score 95;
23.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUID:90255798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----HIFHSGIPQSLQHLIEDSTLVKVGIGIDGDS 195
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Pred.
                                                                                                     SNYCDVMHIFHSGIPQSLQHLIED-STLVKVGIGID 192
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                                   -LFHDYGVSIKDVED----LSDLANQKIGGD
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No. 2
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                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
269
                                   223
                                                                      209
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dynein beta heavy chain - Tetrahymena thermophila
C:Species: Tetrahymena thermophila
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBdA;Molecule type: DNAA;Residues: 1-4589 <LIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: T14914
R;Lincoln, L.M.; Gibson, T.M.; Asai, D.J.; Forney, submitted to the EMBL Data Library, June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: dynein C; Keywords: P-loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Genetic code: SGC5
A; Introns: 286/3; 666/3; 4360/2; 4535/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; \mbox{Description: A gene knockout reveals that dynein beta $A; \mbox{Reference number: } Z18264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AF072878; NID:g5209335; PID:g3309593; PIDN:AAC26117.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: T14914
                                                                                                                                                                                                                                                                                                                                                                             Best
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                                                                                                                                                                                                                                                                                                                                                              Matches
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673
                                 245
                                                                       615
                                                                                                          193
                                                                                                                                              574
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                                                                                                                                                                                                                                                                                     463 VQAFTSVSYDIMNIAEKKFDDDFYEFRSKIKELERRLASVITQGFDDYDTIYGRFKL---
                                                                                                                                                                                                                                                     85
                                                                                                                                                                                                                                                                                                                       42 VQATTSV------HGHEEDPNQIPNNIR---RQLPRSITS----STSYKRFPLSRC
                                                                                                                                                                                                                                                                                                                                                                             Local
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LVRLLKEVKYFLLLRLEVPTTAKDIYTKAETYR
                                                                                                                                                                                                                  -----LDNFEGLLTRPIIADELEKKHIVLLEMYKQDLKQVQSIFLEGKQFVDSMHENAP
                                                                                                                                                                                                                                                   RARNFPAMRFGGRILYSKTATEVDKRAMQLIKVL--DTKRDES----GIAFVGLDIEWRP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X
                               RIR-LGNWEFYPLSKQQLQYAATDAYASWHLYK 276
                                                                   YKDVQKLYTSITKSIKDYEDQKILSWEKEVEDSSQD--KLKQTLLCKDENDLIKVNFDPS
                                                                                                     -GDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCK----ELLK----PN
                                                                                                                                                                              SFRKGVLPGKVATVQICVDSNYCDVMHIFHSGIPQSLQHLIED -- STLVKVGIGID -- --
                                                                                                                                                                                                                                                                                                                                                             68;
                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                            6.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 chain,
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                                                                                                                                                                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ciliary
                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                             No.
                                                                                                                                                                                                                                                                                                                                                                                              95;
705
                                                                                                                                          -KSLRDRIQEPIEKLAQLGQGITEREE
                                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                           97;
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                                                                                                                                                                                                                                                                                                                                                           ; 83
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                                                                                                       244
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RESULT 15 C71620

A; Experimental source: C; Genetics: A; Gene: PFB0215c A;Status: preliminary; A;Molecule type: DNA A;Residues: 1-416 <GAR> R;Gardner, M.J.; Tettelin, H.; Pertea, M.; Salzberg, S.; Science 282, 1126-1132, 1998 protein with Egl-like 3'.5' exonucl. domain PFB0215c - malaria parasite (Plasmodium C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000 C;Accession: C71620 A;Cross-references: GB:AE001381; A;Experimental source: clone 3D7 A; Accession: C71620 A; Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum A; Reference number: A71600; MUID:99021743Tettelin, H.; Carucci, D.J.; alzberg, S.; Zhou, L.; Sutton nucleic .; Zhou, L.; acid GB:AE001362; sequence , D.J.; Cummings, L.M.; Aravind, L.; Koonin, Sutton, G.G.; Clayton, R.; White, O.; Smith, not NID:g3845124; PIDN:AAC71832.1; PID:g384 shown; translation not ж.

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title: .
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein -
      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_AA:*
1: /cgn2_6/ptodata/1
2: /cgn2_6/ptodata/1
3: /cgn2_6/ptodata/1
4: /cgn2_6/ptodata/1
5: /cgn2_6/ptodata/1
6: /cgn2_6/ptodata/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-896-186B-24
1491
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   Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/Packfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
   GenCore version (c) 1993 - 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
US-08-781-891-71
US-09-127-670-6
US-09-1281-891-206
PCT-US94-00198-4
US-09-722-139-2
US-09-99-845-2
PCT-US93-11298-2
US-08-990-166-12
US-08-990-571-34
US-08-990-571-34
US-08-990-571-34
US-08-990-571-37-1
US-07-997-133-1
US-07-997-133-1
US-08-441-944A-4
US-08-451-622A-12
US-08-451-622A-12
US-08-451-622A-12
US-08-451-706-2
US-08-687-289A-7
US-08-687-289A-7
US-08-687-289A-8
US-08-687-289A-8
US-08-687-289A-8
US-08-687-289A-8
US-08-687-289A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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(without alignments)
541.121 Million cell upd
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 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
771 Appl
5 (6) Appl
2 (6) Appl
2 (7) Appl
2 (7) Appl
3 (7) Appl
4 (7) Appl
5 (7) Appl
6 (7) Appl
7 (7) Appl
7 (7) Appl
7 (7) Appl
7 (7) Appl
8 (7) Appl
9 (7) Appl
9
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Qy

88

NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG: | : | | | | :| | : : | | | |

Query Match 23.6%; Score 352; DB 3; Length Best Local Similarity 37.7%; Pred. No. 7.3e-30; Matches 75; Conservative 41; Mismatches 75; Inde	US-08-781-891-71 US-08-781-891-71 US-08-781-891-71 ISEQUENCE 71, Application US/08781891 PACENT NO. 6090520 GENERAL INFORMATION: APPLICANT: FL, Ying-Hui APPLICANT: VU, Chang-En APPLICANT: VU, Chang-En APPLICANT: Willigan, John T. APPLICANT: Milligan, John T. APPLICANT: Milligan, John T. APPLICANT: Milligan, John T. APPLICANT: Schellenberg, Gerald D. TITLE OF INVENTION: WERREY SYNDROME TITLE OF INVENTION: WERREY SYNDROME UMBER OF SEQUENCES: 209 CORRESPONDENCE ADDRESS: ADDRESSEE: SEED and BERRY LLP STREET: 6300 COlumbia Center, 701 Fifth Avenue CITY: Seattle STATE: Washington COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: LBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: PACENTIN Release #1.0, Version #1.30 CURRENT APPLICATION NAMER: PC-DOS/MS-DOS SOTTWARE: PACENTIN Release #1.0, Version #1.30 APPLICATION NUMBER: US/08/781,891 FILING DATE: 27-DEC-1996 CLASSIFICATION NUMBER: 39,317 REFERENCE/DOCKET NUMBER: 30,317 REFERENCE/DOCKET NUMBER: 30,300/30/30/30/30/30/30/30/30/30/30/30/30/	ALIGNMENTS	28 75.5 5.1 1078 1 US-08-484-565-7 29 75.5 5.1 1078 2 US-08-480-751-7 30 75.5 5.1 1078 2 US-08-943-986-7 31 75.5 5.1 1078 3 US-08-353-784-7 32 75.5 5.1 1078 3 US-08-484-7198-7 33 75.5 5.1 1078 4 US-08-484-7199-7 34 75.5 5.1 1088 1 US-08-485-588-6 35 75.5 5.1 1088 2 US-08-480-751-6 36 75.5 5.1 1088 2 US-08-480-751-6 37 75.5 5.1 1088 2 US-08-943-986-6 38 75.5 5.1 1088 3 US-08-480-751-6 40 75.5 5.1 1088 3 US-08-484-7198-6 40 75.5 5.1 1088 3 US-08-484-7198-6 41 75.5 5.1 1088 4 US-08-484-7198-6 42 75 5.0 1385 1 US-07-876-280-2 43 75 5.0 1385 1 US-07-775-772-2 45 75 5.0 1385 1 US-08-063-770-2 45 75 5.0 1385 1 US-08-063-770-2
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US-09-127-670-6
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                                                                                                                                                     Sequence 206, Applicate Patent No. 6090620 GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ASSAYS FOR COMPOUNDS WHICH EXTEND LIFE TITLE OF INVENTION: SPAN FILE REFERENCE: MIT-7720PA CURRENT APPLICATION NUMBER: US/09/127,670 CURRENT FILING DATE: 1998-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Massachusetts Institute
APPLICANT: Leonard P. Guarente
APPLICANT: David A. Sinclair
APPLICANT: David B. Lombard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: US 60/054,629 EARLIER FILING DATE: 1997-08-04
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                     TITLE OF INVENTION:
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     NUMBER
                                                              APPLICANT:
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     OF.
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Fu, Ying-Hui
Yu, Chang-En
Oshima, Junko
Mulligan, John T.
Schellenberg, Gerald D.
Schellenberg, Gerald D.
VENTION: GENE AND GENE PRODUCTS RELATED TO
VENTION: WERNER'S SYNDROME
EQUENCES: 209
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36.6%; Pred. No. 2e-28;
tive 42; Mismatches 72; Indels
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PCT-US94-00198-4
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INFORMATION FOR SEQ ID NO: 5EQUENCE CHARACTERISTICS:
LENGTH: 1401 amino acids
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                   CURRENT APPLICATION DATA:
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                                    COMPUTER: Macintosh
OPERATING SYSTEM: 6.0.8
SOFTWARE: Microsoft Word 5.1a
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STATE: Washing
                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/781,891 FILING DATE: 27-DEC-1996
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 PCT/US94/00198
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Pred. No. 2e-27;
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Length 1401; Indels 14;

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US-09-722-139-2
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SEQ ID NO 2
LENGTH: 1375
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                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6355471el motor proteins and
TITLE OF INVENTION: their use
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09722139 Patent No. 6355471
                                        Matches
                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/722,139
CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (201)822-7039 INFORMATION FOR SEQ ID NO:
                                                                                                                                                         TYPE: PRT
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)822-7255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2029 NIETSTAYSPSVHESTSSEGIPIITLTMSNF-----SDRHVDIDTVAYKFLQIY 2077
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ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2132 FMDNYGKCLDKDNYYVSSKIPHYFINSNSDEGLMK-SVGITGQGLKVLQDIRVSLHDITL 2190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2078 ARIWTTKHCLIIDCTEFDEG----GLDMRKFISLVMGLLP-EVAP-KNCIGCYYFNVNET 2131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 SITSSTSY-----KREPLSRCRARNFPAMREGGRILYSKTATEVDKRAMQLIK-- 116
13 EEELLAIDAIEASYNFSRSSSSSSSSAAPTVQATTSVHGHEEDPNQIPNNIRRQLPRSITS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 6.2%; Score 93; DB 5; Length 3079; Local Similarity 19.3%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lunn, Paul G. REGISTRATION NUMBER: 32,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F-----HSGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVED 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSDLANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------VLDTKRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHI 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3079 amino acids
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                             1055
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15-JAN-1993
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19.0%;
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                                      52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DX0352 PCT
                                  Score 87.5; DB 4;
Pred. No. 2;
2; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---FTPVSLKIGDIYFQVLHETPRQYKIRD 2224
                                                                        Length 1375;
                                      Indels
                                                                                                                                                                                                                                                                                                                                 methods for
                                      79;
                                    Gaps
                                      13;
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                                                                                                            ; TOPOLOGY: US-07-989-845-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/07989845 Patent No. 5304472 GENERAL INFORMATION:
                                      Matches
                                                      Query Match
Best Local
                                                                                                                                                                                  TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEPHAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HASSAK, Janet E.
REGISTRATION NUMBER: 28,616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1188 IPDLV 1192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Swartz, James TITLE OF INVENTION: METHOTITLE OF INVENTION: PRODUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bass, Steven APPLICANT: Swartz, Jame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166
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935 KEEQLA----
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ZIP: 940
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CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: U. FILING DATE: 19921120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73
 86 ARNFPAMRFGGRILYSKTATEV------DKRAM---
                                                                                                                                                 TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAE-QEALEKDQERLEYEIQQLKQKIYEVDGVQKDHHGTLEGKVASSSLPVSAEKSHLVP 1095
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                                                        Similarity
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                                                                                                                                                                  348 amino acids
                                      Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                      5.8%;
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                                      34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 Kb floppy disk
                                                      Score 86.5;
Pred. No. 0
                                      Mismatches
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                                                                       DB
                                    73;
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                                                                       Length 348;
                                    Indels
-QLIKVLDTKRDESG 126
                                    97;
                                    Gaps
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                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                         TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                      ATTORNEY_AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERNCE/DOCKET NUMBER: 752
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: METHOD OF TITLE OF INVENTION: BACTERIA NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS: Genentech, Inc.
                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
     166
                               127 IAFV-----GLDIEWRPSFRKGV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 TSFVFTSYLAKVNEEWKNNVGTGSTVKWPIGLGGKGNDGIAAFVQRLPGAIGYVEYA---
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                                                                                                                                                                                                                                                                            TELEFAX: 415/77168
                                                                                                86
                                                                                                                                             Local Similarity
                                                                                                                                                                                                                            LENGTH: 348 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                             TELEPHONE: 415/252-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 460 Point San Bruno CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
TSFVFTSYLAKVNEEWKNNVGTGSTVKWPIGLGGKGNDGIAAFVQRLPGAIGYVEYA---
                                                                                               ARNFPAMRFGGRILYSKTATEV-----DKRAM---
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                                                               AVNIPGLKSGELVLDGKTLGDIYLGKIKKWDDEAIAKLNPGLKLPSQNIAVV-RRADGSG
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                                                                                                                                Conservative
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                                                                                                                                                                                                               linear
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                                                                                                                                             5.8%; Score 86.5; D
20.9%; Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHOD OF CONTROLLING POLYPEPTIDE PRODUCTION
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                                                                                                                              34;
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                                                                                                                                Mismatches
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                                                                                                                                                            ВG
                                                                                                                              73;
                                                                                                                                                            5.
                                                                                             ---QLIKVLDTKRDESG 126
                                                                                                                                                           Length 348;
                               --LPGKVATVQICVDS 158
                                                                                                                              Indels
                                                                                                                              97;
                                                                                                                             Gaps
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Best Local Similarity 21.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/08/907,166
CURRENT FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 574
                                                                                                                                                                                                                                                                                                                 Sequence 34 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Applical Patent No. 5948666 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT: Mather, Eric
TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF NOVEL POLYMERASES
FILE REFERENCE: 09010/027001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                   APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOU
                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                    APPLICANT:
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STATE: Washington
                                                                                         COUNTRY:
                                                                                                                                      STREET:
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                                                                                                                                                       ADDRESSEE:
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6183976
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                                                                                                                                      6300 Columbia Center,
                                                                                         USA
                                                                                                                                                                                                                                                  Reed, Steven G.
Lodes, Michael J.
Houghton, Raymond
                                                                                                                                                        SEED AND BERRY
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21.9%; Pred. No.
                                                                                                                                                                                                     COMPOUNDS AND AND TREATMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                         701 Fifth Avenue
                                                                                                                                                                                                     OF B. MICROTI INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                               281
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3.5;
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RESULT 10
US-08-990-571-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (206) 622-4900
TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                           SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
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REFERENCE/DOCKET NUMBER:
                                                                              CLASSIFICATION:
                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                           ZIP: 98104
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REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/845,258 FILING DATE: 24-APR-1997
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N: 435
                                                                                                11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                         Steven G. et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.3%; Score 79.5; DB 4; 22.4%; Pred. No. 2.5; tive 35; Mismatches 106;
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                                                                                                                 us/08/990,571
210121.426C2
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RESULT 11
US-08-723-142A-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6306396 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34,
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Best Local Similarity 22.4%;
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INFORMATION FOR SEQ ID NO:
              INFORMATION FOR SEQ
                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
NAME: Maki, David J.
31,392
                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
ZIP: 98104
                                                                                           REGISTRATION NUMBER: 31
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                             APPLICATION NUMBER: US/08/723,142A FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6300 CCITY: Seattle
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                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
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CHARACTERISTICS:
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                                   (206)682-6031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lodes, Michael J
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                  ID NO:
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Pred. No. 2
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RESULT 12
US-08-895-601-6
; Sequence 6, Ap
; MOLECULE TYPE: US-08-895-601-6
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Best Local :
                                                                                                TELEFAX: 617-832-7000 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 617-832-1000
                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: REGULATION OF KAPPA B (IKB) DEGRADATION, TITLE OF INVENTION: AND METHODS AND REAGENTS RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Glass, Susan J.
APPLICANT: Rolfe, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                   TYPE: a
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                                                                                                                                                              REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-096.01
                                                                                                                                                                                                                                        CLASSIFICATION:
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                                   TOPOLOGY:
                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                     NAME: Vincent, Matthew P.
                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/895,601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESGI--AFVGLDIEWRPSFRKG---VLPGKVATVQICVDSNYCDVMH-IFHSGIPQSLQH 177
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Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                           Version #1.30
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US-07-640-029-2
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Best Local Similarity
Matches 63; Conserv
                                                                                                                 TELEFAX: 510-655-3542 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0; Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/640,029
FILING DATE: 19910111
TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 4300
CITY: Emeryville
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Expression and Use of TITLE OF INVENTION: Growth Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                   STRANDEDNESS:
                                                                                                                                                TELEPHONE:
                                                                                                                                                                                          REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: CH-165
                                                                                                                                                                                                           NAME: McClung, Barbara G
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
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                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                          LENGTH:
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                                                      AMINO ACID
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Barr, Philip J.
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                     linear
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RESULT 14
US-07-997-133-1
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Best Local
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                              TELEX: 248855 OPAT UR INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5288855man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 769-2:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sarmientos, Paolo
TITLE OF INVENTION: Extracellular Form of the Human
TITLE OF INVENTION: Fibroblast Growth Factor Receptor
                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Relicurrent APPLICATION DATA:
                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                   STATE: VI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 SDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYT 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 VPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVY
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                                                                              TELEFAX:
                                                                                                                                                                                                      APPLICATION NUMBER: US/07/642,755 FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                      FILING DATE: 28 CLASSIFICATION:
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/07/997,133
FILING DATE: 28-DEC-1992
                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1755 Je
CITY: Arlington
                                                                                              TELEPHONE:
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              LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                           Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1755 Jefferson Davis Highway, Fourth Floor
              822 amino acids
                                                                                : (703)521-4500
(703)486-2347
                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mazue, Guy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isacchi, Antonella
Roncucci, Romeo
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                                                                                                                                    769-226-0
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                                                                                                                                                                                                                                                                                                                          Version
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RESULT 15
US-07-921-807B-4
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Best Local Similarity
"atches 56; Conserva
; TOPOLOGY: 1:
; MOLECULE TYPE:
US-07-921-8078-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-07-997-133-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Applic Patent No. 5474914 GENERAL INFORMATI
                                                                                                             TELEFAX: (510) 655-35
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDLIM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                          TELEFONMUNICATION INFORMATION: TELEFHONE: (510) 601-2708
TELEFAX: (510) 655-3542
                                                                                                                                                                                                                          FILING DATE: 29-SEP-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ALPSSEDDDDDDDSSSEEK----ETDNTKPNRMPVAP-----YWTSPEK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 DLANQKIG 221
                                                                                                                                                                              NAME: McCLUNG, BARBARA G. REGISTRATION NUMBER: 33,1 REFERENCE/DOCKET NUMBER:
                                              STRANDEDNESS:
                                                                TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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                                                                            LENGTH:
                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSSSNWIDDA-------FTEEELLAIDAIEASYNFSRSSSSSSAAPT----VQATT 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                           4: 822 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Emeryville
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                                                                                                                                                                                                                                                                                                                                                                                                                               CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: CHIRON CORPORATION
4560 Horton Street - 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPAETE, RICHARD
VENTION: METHOD OF INCREASING EXPRESSION
VENTION: OF VIRAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                             USA
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18.2%;
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Pred. No. 8.9;
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                                                                                                                                                                                                                                                                                                              Version
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rch tim	ω	2	2	ь	N	1	1	1	_				Query Match Best Local Matches 5
e	11	14	81	73	21	59	61	0.7	12	47	61	Ľ	es Loc Ma
Search completed: October 31, 2002, 13:43:34 Job time : 19 secs	341 CLAGNSIG 348	214 DLANQKIG 221	281 SDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNTTDKENEVLHLRNVSFEDAGEYT 340	QSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLS 213	221 VPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVY 280	159 NY 172	161 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV 220	107 VDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPGKVATVQICVDS- 158	121 ALPSSEDDDDDDSSSEEKETDNTKPNRMPVAPYWTSPEK 160	SVHCHEEDPNQIPNNIRRQLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATE 106	61 VQSINWLRDGVQLAESNRTRITGEEVEVQDSVPADSGLYACVTSSPSGSDTTYFSVNVSD 120	MSSSNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSSAAPTVQATT 46	Query Match 5.3%; Score 78.5; DB 1; Length 822; Best Local Similarity 18.2%; Pred. No. 8.9; Matches 56; Conservative 46; Mismatches 99; Indels 107; Gaps 11;

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
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                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to I score greater than or equal to the score of the result being and is derived by analysis of the total score distribution
  1491
1433
1028
996
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                                                                                                                                                                                                                                                                   Score
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seq length: 2000000000
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1: /SIDSI/gcgdata/ge
2: /SIDSI/gcgdata/ge
3: /SIDSI/gcgdata/ge
4: /SIDSI/gcgdata/ge
6: /SIDSI/gcgdata/ge
6: /SIDSI/gcgdata/ge
7: /SIDSI/gcgdata/ge
8: /SIDSI/gcgdata/ge
9: /SIDSI/gcgdata/ge
10: /SIDSI/gcgdata/ge
11: /SIDSI/gcgdata/ge
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12: /SIDSI/gcgdata/ge
13: /SIDSI/gcgdata/ge
14: /SIDSI/gcgdata/ge
15: /SIDSI/gcgdata/ge
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25: /SIDSI/gcgdata/ge
26: /SIDSI/gcgdata/ge
27: /SIDSI/g
    100.0
100.0
96.1
68.9
66.8
60.1
23.6
22.7
22.7
22.7
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Gapop 10.0 , Gapext 0.5
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1491
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Match Length DB
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Mouse WRN gene pro
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ALIGNMENTS

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DE Arabidopsis thaliana protein fragment SEQ ID NO: 67237.

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Protein identification; signal transduction pathway; metabolic pathway; kw hybridisation assay; genetic mapping; gene expression control; promoter; XX

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Arabidopsis thaliana.

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EP1033405-A2.

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06-SEP-2000.

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25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 23-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0128744.
PR 01-APR-1999; 99US-0128744.
PR 01-APR-1999; 99US-012874.
PR 01-APR-1999; 99US-012874.
PR 10-APR-1999; 99US-012874.
PR 11-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130049.

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                                                                     06-SEP-2000.
                                                                                           EP1033405-A2
                                                                                                              Arabidopsis thaliana
                                                                                                                                     termination sequence
                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                Arabidopsis thaliana
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Pred. No. 4.6e-151;
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RESULT 3
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                      Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
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RESULT 4
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AC AAG5
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05-MAR-1999,
09-MAR-1999,
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990S-01511930
990S-0151930
990S-0153758
990S-0153758
990S-0154779
990S-0155486
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990S-0159331
990S-0159331
990S-0160980
990S-0160980
990S-01614044
990S-0161359
                  288
 197
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Pred. No. 1.1e-101;
0; Mismatches 0;
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RESULT 5 AAG24978

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99US-0139455. 99US-0139455. 99US-0139456. 99US-0139457. 99US-0139459. 99US-0139459.	99US-0139119. 99US-0139452. 99US-0139453. 99US-0139492.	99US-0138094. 99US-0138540. 99US-0138847.	99US-0137528. 99US-0137502. 99US-0137724.	99US-0136392. 99US-0136782. 99US-0137222.	99US-0135629. 99US-0136021.	99US-0134941. 99US-0135124. 99US-0135333.	99US-0134370. 99US-0134768.	99US-0134221. 99US-0134221.	99US-0134256. 99US-0134276.	99US-0132486. 99US-0132487.	99US-0132484. 99US-0132485.	9905-0132448. 9905-0132407.	9905-0130891. 9905-0130891. 9905-0131449	99US-0130077. 99US-0130449.	99US-0128714. 99US-0129845.	99US-0127462. 99US-0128234.	9905-0126705. 9905-0126705.	99US-0123548. 99US-0123548.	99US-0121825.	2000EP-0301439.			thaliana.	assay; genetic mapping; gene express quence.	fication: signal transduction pathway: metabolic	protein fragment cen II No.	first patrol	AAG24978 standard; Protein; 197 AA.
																						<u>.</u>						
יי סי סי סי קיי א א א א א א א א א א	ק אק אק	PR PR	PR PR	מ א א	PR	ק אמ א	PR	א ק א ק	מ ק ק	PR PR	PR	PR	י טי ט ג ג ג	PR	PR PR	PR	אַק אַק	מי געט	PR	PR	PR	PR	PR	PR	י גלי	PR	p P ?	PR PR
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Query Match 66.8
Best Local Similarity 97.0
Matches 191; Conservative
                                                                                                   VQICVDSNYCDVMHIFHSGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDVQICVDNNYCDVMHIFHSGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDV
                                                                                                                                                             WHLYKVLKDLPDAVSGS 288
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; Pred. No. 2.9e
2; Mismatches
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                                                                                                                                                                                                                                                    Length 197;
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05-MAR 1999
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152 61

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232
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                                                                                       / Match 60.1%;
Local Similarity 96.6%;
hes 171; Conservative
                  61
                                                     <u>بــ</u>
                PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGBKKWGLASL
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99US-0161406.
                                                                                      Score 896; DB 21;
Pred. No. 1.3e-87;
2; Mismatches 4;
                                                                                                          Length
                                                                                        Indels
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                                                                                        Gaps
                                                      60
                   120
                                    231
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18-JUN-1999
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99US-0144334.
99US-0144332.
99US-0144332.
99US-014638.
99US-0147951.
99US-014638.
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99US-014795.

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Best Local S
Matches 75
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29-DEC-1995;
29-DEC-1995;
30-JAN-1996;
30-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the human WRN gene product which is associated with Werner's syndrome. The products can be used for the detection and treatment of Werner's syndrome (WS), an autosomal recessive disorder with a complex phenotype, as well as related diseases.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecule encoding the WRN gene product useful for detection and treatment of Werner's syndrome, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAX83001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DARW-) DARWIN MOLECULAR CORP
(OSHI/) OSHIMA J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recessive disorder; phenotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human WRN gene product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-AUG-1999 (first entry)
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                                       216
                                                                        267
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                                       DAYAGFIIYRNLEILDDTV 234
                                                      DAYASWHLYKVLKDLPDAV
                                                                                                KVATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSI 206
                                                                                                                                                                                                                                             DLPFLEFTGSIVYSYDASDCSFLSE-----DISMSLSDGDVVGFDMEWPPLYNRGKL-G
                                                                                                                                                                                                                                                                              NFPAMRFGGRILYSKTATEVDKRAMQLIKVLDTKRDESGIAFVGLDIEWRPSFRKGVLPG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1997-363671/33.
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                                                                                                                                                                        KVALIQLCVSESKCYLFHVSSMSVFPQGLKMLLENKAVKKAGVGIEGDQWKLLRDFDIKL
                                                                                                                                                                                                                                                                                                                    Similarity 75; Conserv
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95US-0009409.
95US-0580539.
96US-0010835.
96US-0594242.
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                                                                    285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                ; Score 352; DB 18;
; Pred. No. 6.3e-28;
41; Mismatches 75;
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AAW97841
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                              mWRN gene; l
life span;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a novel mouse WRN helicase protein which is associated with Werner's syndrome. The mouse WRN gene is useful for the diagnosis of human Werner's syndrome.
Mus sp
                                                                                   Murine mWRN polypeptide (WRN homologue).
                                                                                                                       07-JUN-1999
                                                                                                                                                          AAW97841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 18-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mouse gene encoding protein - used for Werner's syndrome
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N-PSDB; AAV35114, A
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                                                                                                                                                                                          AAW97841 standard; Protein; 1401
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                                                                                                                                                                                                                                                                                                                                                                                                                    K---VATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYG 203
                                                                                                                                                                                                                                                                              AATDAYAGLIIYQKLGNLGDTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74;
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                                WRN gene; homologue; Werner's syndrome; ageing.
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Pred. No. 1.5e-26;
2; Mismatches 72;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells, accumulation of ribosomal circular DNA is responsible for age-related enlargement and fragmentation of the nucleolus. A mutation in the yeast MRN homologue SGSI causes premature ageing, suggesting a common ageing mechanism in all eukaryotes. Insight into the ageing process in model systems can provide insight into
                  31-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-153773/13
N-PSDB; AAX24302.
                                                 AAY14519;
                                                                                AAY14519 standard;
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                                                                                                                                                                                                                                                                                            KRSRVAVIQUCVSENKCYLFHISSMSVFPQGLKMLLENKSIKKAGVGIEGDQWKLLRDFD
                                                                                                                                                                                                                                                                                                                K---VATVQICVDSNYCDVMHIFHSGI-PQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYG
                                                                                                                                                                AATDAYAGLIIYQKLGNLGDTV
                                                                                                                                                                                                                               VKLESFYELTDVANEKLKCAETWSLNGLVKHVLGKQLLKDKSIRCSNWSNFPLTEDQKLY
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                                                                                Protein;
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Pred. No. 1.5e-26;
2; Mismatches 72;
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RESULT 11
ABB71575
ID ABB71
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Best Local Similarity
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29-DEC-1995;
29-DEC-1995;
30-JAN-1996;
30-JAN-1996;
                                                                                                                                                                                                                                                                                                                                           This sequence represents the mouse WRN gene product. The corresponding human gene product (AAY14517) is associated with Werner's syndrome. The products can be used for the detection and treatment of Werner's syndrome (WS), an autosomal recessive disorder with a complex phenotype, as well as related diseases.
                 Drosophila melanogaster polypeptide SEQ ID NO 41517
                                      26-MAR-2002
                                                         ABB71575
                                                                            ABB71575 standard; Protein;
                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Fig 6; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecule encouseful for detection and treatment
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95US-0009409.
95US-0580539.
96US-0010835.
96US-0594242.
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                                                                                                                                                                                                                                                                                    22.1%; Score 330; DB 18; 36.0%; Pred. No. 1.4e-25; tive 43; Mismatches 71;
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                                                                                                                                                283
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                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding the WRN gene product ment of Werner's syndrome, and
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developmental biology; cell

signalling; insecticide;

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RESULT 12
ABB62653
ID ABB62
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AC ABB62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic a
genes from Drosophila
interactions -
             26-MAR-2002
                                        ABB62653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 41517; 21pp + Sequence Listing; English.
                                                                 ABB62653 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent
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N-PSDB; ABL15678.
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                   YRELE 305
                                                                                                                                                           YKVLK 279
                                                                                                                                                                                     WCNEVCETGGRWSLERLTNFIAKKAMDKSKKVRMSKWHVIPLDENQLMYAAIDVYIGQVI
                                                                                                                                                                                                                                       CYIYQLTNVKKLPAALVALINHPKVRLHGVNIKNDFRKLARDFPEVTAEPLIEKCVDLGL
                                                                                                                                                                                                                                                               CDVMHIFH-SGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDY-----GVSIKDVEDLSD 214
                                                                                                                                                                                                             LANQKIGGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHL 274
                                                                                                                                                                                                                                                                                          FTESQDIAASADDVLQWVEKQKDE--VVPMAFDMEWPFSFQTG--PGKSAVIQICVDEKC
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Pred. No. 9.7e-16;
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                                                                                                                                                                                                                                                                           QΥ
                                                                                                                                                                                                                                                                                                        DЪ
                                                                                                                                                                                                                                                                                                                             Qy
Environmental stress tolerant protein
                          02-MAY-2001
                                                                             AAB80638 standard; Protein;
                                                    AAB80638
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Query Match
Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABLIG511), expressed DNA sequences (ABLIG1840-ABLIG6175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventuageful in developmental biology and in elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 14751; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABL06756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                   (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interactions
                                                          167
                                                                                                                                                    162
                                                                                                                                                                                                               109
227
                            280
                                                                                                                     109
                                                                                                                                                                                  71
                 _ E
                                                                            GGDKKWGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLY-KVLK
                                                                                                                                                                                                   KRAMQLIKVLDTKRDESGIAFVGLDIEW-------RPSFRKGVLPGKVATVQICVDSNYC
DΓ
                                                                                                                     ALFRLCHMKQIPQDLRELLEDDSVIKVGVAPQEDAMKLSHDYGVGVASTLDLRFLC--VM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-656860/75
                                                          AGHKPEGLGKLSKTHLNYTLDKHWRLACSNWEAKTLEPKQLDYAANDALMAVAIYQKLCR
                                                                                                                                                DVMHIFH-SGIPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKI 220
                                                                                                                                                                                KNHCQTFKVL-----GFDCEWITVGGSRRP-----VALLQLSSHRGLC
                              281
                                                                                                                                                                                                                                                                                                        583 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M,
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                          14.3%;
33.5%;
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                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                          Score 212.5;
Pred. No. 1.
                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                           .4e-13;
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                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                    format directly from WIPO
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                         Length 583;
                                                                                                                                                                                                                                           33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reagent
e invention
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6,

(first entry)

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB80608 - AAB80639, which impart environmental stress resistance. The chivention relates to a method for identifying DNA encoding proteins imparting environmental stress resistance. The method comprises inserting color imparting environmental stress resistance. The method comprises inserting color from a library originating in a salt-resistant organism into a host cell, culturing the transformants under conditions in which the cuntransformed host does not grow well, and selecting for viable clones. The method is useful for obtaining DNA encoding environmental stress resistance factors. The DNA encoding proteins conferring environmental stress resistance, can be used in the production of plants resistant to environmental stress, which can be cultivated in unfavourable environments such as deserts, salt damaged ground, cold regions and the coeans. They can be used for increasing the area of land covered by green plants, and desert greening and afforestation, in order to counter the effects of the increase in atmospheric carbon dioxide concentration. PCR primers AAF74219 and AAF74220 are used in an example illustrating the
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening method to obtain DNA encoding environmental stress resistance factor, useful for producing transgenic plants resistant to
 Human
                                   11-JAN-2002
                                                                                                     ABB11264 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              environmental stress
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUL-1999; 99JP-0235910.
24-MAR-2000; 2000JP-0085377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salsola komarovii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Environmental stress resistance; salt; heat; desert; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide sequences AAF74187 - AAF74218 encode proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NISC-) JAPAN SCI & TECHNOLOGY
                                                                                                                                                                                          163
                                                                                                                                                                                                                                                           108
                                                                                                                                                                                                                                                                                             189
                                                                                                                                                                                                                                                                                                                                                             130 VGLDIEWRPSFRKGVLPGKVATVQICVDSNYCDVMHIFHS-GIPQSLQHLIEDSTLVKVG 188
                                                                                                                                                                                                                                                                                                                               55
                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                      KVMLSGWDQYCLSNDQVQYACVDAYVSLRL
                                                                                                                                                                                                                      RIRLGNWEFYPLSKQQLQYAATDAYASWHL
                                                                                                                                                                                                                                                                                          I--GIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLV--CKELLKPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-147355/15
DB; AAF74217.
                                                                                                                                                                                                                                                          VHNGRARDLLQGSHHE----LDVNNLVDLAEEENGHYLKWSMEDMAEDVLGFC-GVHKPR
                                                                                                                                                                                                                                                                                                                             IGLGVQWKPS-----STSAATLQLSIDKK-CLIFQLSHSPATPATLRDLLLDDRVTFFG
secreted protein homologue, SEQ ID NO:1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64; Page 159-160; 167pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ozeki Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 AA;
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                 (first entry)
                                                                                                   peptide;
                                                                                                                                                                                                                                                                                                                                                                                                               12.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito
                                                                                                                                                                                                                                                                                                                                                                                                28;
                                                                                                     127
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 178.5;
Pred. No. 1.
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3; Mismatches
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                                                                                                                                                                                                                          274
                                                                                                                                                                                                                                                                                                                                                                                             1.7e-10;
hes 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                         107
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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoissis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vascuropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.
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Homo sapiens.

WO200157188-A2.

09-AUG-2001

05-FEB-2001; 2001WO-US03800.

03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;

WPI; 2001-457740/49 N-PSDB; ABA08508.

aim 20; Page 161; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA05734 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host calls comprising a nucleotide of the invention, methods of producing the novel polypeptides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities; stem cell growth factor activity; haematopoiesis regulatory activity; tissue growth activity; haematopoiesis regulatory activity; tissue growth activities; or may be involved in oncogenesis, cancer cell proliferation or cell thrombolytic activities; receptor or ligand activities; or may be invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, heamatopoietic disorders (e.g., myeloid or lymphold cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative rethinpathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with bacterial and fungal infections in addition to immune disorders. Polypeptides with factor activity may be used to promote to augment or replace cells damage by and nucleotides that can be used to augment or replace cells damage by allness, end of cells and of cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damage by allness.

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AAY29336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 41
         activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopolesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatiand thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful
                                                                                                                The present sequence represents a human secreted protein. Human secreted protein polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional
                                                                                                                                                                                                                                            New polynucleotides encoding secreted human proteins derived from, e.g. fetal brain potentially used as immunostimulators.
                                                                                                                                                                                                                                                                                         WPI; 1999-458682/38
N-PSDB; AAX90441.
                                                                                                                                                                                                                                                                                                                                       Agostino MJ, Clark
Jacobs K, Lavallie
Treacy M, Wong GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.
                                                                                                                                                                                                               Disclosure; Page 133-134; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JAN-1999;
22-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9937674-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    haematopoiesis regulation; chemotactic; chemokinetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY29336 standard; Protein; 147 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein clone cs756_2 alternate reading frame
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 IPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLA-----NQKIGGDKK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 WGLASLTETLVCKELLKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKVLKDLP 282
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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  secreted protein; nutrition; cytokine; entiation; immune stimulating; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invasion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0235609.
98US-0072134.
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                                                                                                                                                                                                                                                                                                                                                       ER,
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                                                                                                                                                                                                                                                                                                                                                       McCoy JM, Merberg
                                                                                                                                                                                                                                                                                                                                                                     Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  imulating; vaccine; suppression; gene therapy;
tissue growth; activin; inhibin; cadherin;
haemostatic; thrombolytic; anti-inflammatory;
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Pred. No. 5.4e-08;
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                                                                                                                                                                                                                                                                                                                                                       D,.
                                                                                                                                                                                                                                                                                                                                                                     Fechtel K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell
                                                                                                                                                                                                                                                                                                                                                       Steininger RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 127;
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                                                        haemostatic
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            Search completed: October
                                               В
                                                                                                                                         Matches
                                                                                                                                                               Query Match
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                                                                                                      171 IPQSLQHLIEDSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLA-----NQKIGGDKK 225
                                                          226 WGLASLTETLYCKELLKPURIRLGNWEFYPLSKQQLQYAATDAYASWHLYKYLKDLP
                                               80
                                                                                                                                                    Local
                                                                                           23 LPRTLLDILADGTILKVGVGCSEDASKLLQDYGLVVRGCLDLRYLAMRQRNNLLCNG---
                                             LSLKSLAETVLNFPLDKSLLLRCSNWDAETLTEDQVIYAARDAQISVALFLHLLGYP
                                                                                                                                       41;
38 secs
                                                                                                                                                    Similarity
                                                                                                                                                                                       147
                                                                                                                                         Conservative
                                                                                                                                                                                       AA;
                                                                                                                                                   10.1%;
            31,
            2002,
                                                                                                                                       20;
                                                                                                                                                   Score 151;
Pred. No. 6
             13:41:54
                                                                                                                                         Mismatches
                                                                                                                                                   1; DB 20;
. 6.8e-08;
                                                                                                                                         48;
                                                                                                                                                              Length 147;
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                                                                                                                                       Gaps
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Million (" Maring Marine (- ")